

PTO/SB/64 (09-04)

Approved for use through 07/31/2006. OMB 0651-0031

U.S. Patent and Trademark Office; U.S. DEPARTMENT OF COMMERCE

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DAC
JFW**PETITION FOR REVIVAL OF AN APPLICATION FOR PATENT
ABANDONED UNINTENTIONALLY UNDER 37 CFR 1.137(b)**

Docket Number (Optional)

FORS-04447

First named inventor: Michael W. Kaiser

Application No.: 09/684,305

Art Unit: 1637

Filed: 10/06/00

Examiner: Fredman

Title: IMPROVED CLEAVAGE AGENTS

Attention: Office of Petitions

Mail Stop Petition

Commissioner for Patents

P.O. Box 1450

Alexandria, VA 22313-1450

FAX (703) 872-9306

NOTE: If information or assistance is needed in completing this form, please contact Petitions
Information at (703) 305-9282.

The above-identified application became abandoned for failure to file a timely and proper reply to a notice or action by the United States Patent and Trademark Office. The date of abandonment is the day after the expiration date of the period set for reply in the office notice or action plus an extensions of time actually obtained.

APPLICANT HEREBY PETITIONS FOR REVIVAL OF THIS APPLICATION

NOTE: A grantable petition requires the following items:

- (1) Petition fee;
- (2) Reply and/or issue fee;
- (3) Terminal disclaimer with disclaimer fee - required for all utility and plant applications filed before June 8, 1995; and for all design applications; and
- (4) Statement that the entire delay was unintentional.

1. Petition fee

☒ Small entity-fee \$ 750.00 (37 CFR 1.17(m)). Applicant claims small entity status. See 37 CFR 1.27.

☐ Other than small entity - fee \$ _____ (37 CFR 1.17(m))

2. Reply and/or fee

A. The reply and/or fee to the above-noted Office action in
the form of Amendment and Subst. Sequence Listing in paper and CRF (identify type of reply):

- ☐ has been filed previously on _____
☒ is enclosed herewith.

B. The issue fee and publication fee (if applicable) of \$ _____

- ☐ has been paid previously on _____
☐ is enclosed herewith.

[Page 1 of 2]

This collection of information is required by 37 CFR 1.137(b). The information is required to obtain or retain a benefit by the public which is to file (and by the USPTO to process) an application. Confidentiality is governed by 35 U.S.C. 122 and 37 CFR 1.11 and 1.14. This collection is estimated to take 1.0 hour to complete, including gathering, preparing, and submitting the completed application form to the USPTO. Time will vary depending upon the individual case. Any comments on the amount of time you require to complete this form and/or suggestions for reducing this burden, should be sent to the Chief Information Officer, U.S. Patent and Trademark Office, U.S. Department of Commerce, P.O. Box 1450, Alexandria, VA 22313-1450. DO NOT SEND FEES OR COMPLETED FORMS TO THIS ADDRESS. **SEND TO: Mail Stop Petition, Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.**

If you need assistance in completing the form, call 1-800-PTO-9199 and select option 2.

01/28/2005 SMINASS1 00000037 09684305

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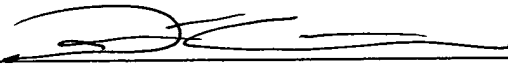
Under the Paperwork Reduction Act of 1995, no persons are required to respond to a collection of information unless it displays a valid OMB control number.

3. Terminal disclaimer with disclaimer fee

- ☒ Since this utility/plant application was filed on or after June 8, 1995, no terminal disclaimer is required.
- ☐ A terminal disclaimer (and disclaimer fee (37 CFR 1.20(d)) of \$ _____ for a small entity or \$ _____ for other than a small entity) disclaiming the required period of time is enclosed herewith (see PTO/SB/63).

4. STATEMENT: The entire delay in filing the required reply from the due date for the required reply until the filing of a grantable petition under 37 CFR 1.137(b) was unintentional. [NOTE: The United States Patent and Trademark Office may require additional information if there is a question as to whether either the abandonment or the delay in filing a petition under 37 CFR 1.137(b) was unintentional (MPEP 711.03(c), subsections (III)(C) and (D)).]

WARNING: Information on this form may become public. Credit card information should not be included on this form. Provide credit card information and authorization on PTO-2038.

<p><u></u> Signature</p> <p><u>David A. Casimir</u> Typed or printed name</p> <p><u>Medlen & Carroll, 101 Howard Street, Suite 350</u> Address</p> <p><u>San Francisco, CA 94105</u> Address</p>	<p><u>1/24/05</u> Date</p> <p><u>42,395</u> Registration Number, if applicable</p> <p><u>608/218-6900</u> Telephone Number</p>
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- Enclosures: ☒ Fee Payment
- ☒ Reply
- ☐ Terminal Disclaimer Form
- ☐ Additional sheets containing statements establishing unintentional delay
- ☐ Other: _____

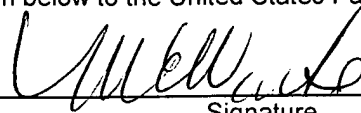
CERTIFICATE OF MAILING OR TRANSMISSION [37 CFR 1.8(a)]

I hereby certify that this correspondence is being:

- ☒ Deposited with the United States Postal Service on the date shown below with sufficient postage as first class mail in an envelope addressed to: Mail Stop Petition, Commissioner for Patents, P. O. Box 1450, Alexandria, VA 22313-1450.

- ☐ Transmitted by facsimile on the date shown below to the United States Patent and Trademark Office as (703) 872-9306.

January 24, 2005
Date


Signature

Mary Ellen Waite
Typed or printed name of person signing certificate



PATENT
Attorney Docket No. **FORS-04447**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Michael W. Kaiser *et al.*
Serial No.: 09/684,305
Filed: 10/06/00
Entitled: **Improved Cleavage Agents**

Group No.: 1637
Examiner: Fredman

**TRANSMITTAL FOR REVIVAL OF AN APPLICATION FOR
PATENT ABANDONED UNINTENTIONALLY UNDER 37 C.F.R. 1.137(b)**

Attention: Office of Petitions
Mail Stop Petition
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

CERTIFICATE OF MAILING UNDER 37 CFR § 1.8(a)

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to the: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450, on **January 24, 2005**.

By: _____

Mary Ellen Waite

Sir or Madam:

Applicants submit for filing in the U.S. Patent and Trademark Office a Petition For Revival Of An Application For Patent Abandoned Unintentionally Under 37 C.F.R. 1.137(b) in the above-identified application. A check in the amount of \$750.00 is enclosed to cover the filing fee for such Petition.

The Commissioner is hereby authorized to charge any additional fee or credit overpayment to our Deposit Account No. 08-1290. **An originally executed duplicate of this transmittal is enclosed for this purpose.**

Dated: January 24, 2005

David A. Casimir
Registration No. 42,395
MEDLEN & CARROLL, LLP
101 Howard Street, Suite 305
San Francisco, California 94105
608/218-6900



PATENT
Attorney Docket No. **FORS-04447**

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: *Michae W. Kaiser et al.*

Serial No.: 09/684,305

Filed: 10/06/00

Entitled: **IMPROVED CLEAVAGE AGENTS**

Group No.: 1637

Examiner: JN Fredman

**AMENDMENT AND
SUBSTITUTE SEQUENCE LISTING**

MAIL STOP PETITION
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8(a)(1)(i)(A)

I hereby certify that this correspondence (along with any referred to as being attached or enclosed) is, on the date shown below, being deposited with the U.S. Postal Service with sufficient postage as first class mail in an envelope addressed to: MAIL STOP PETITION Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.

Dated: 1-24-05

By: [Signature]

Mary Ellen Waite

Sir or Madam:

Please amend the application as follows:

Amendment to the Specification begins on page 2 of this communication.

Remarks are on page 3 of this communication.

AMENDMENT TO THE SPECIFICATION

Please replace the Sequence Listing filed October 6, 2000 with the substitute Sequence Listing attached here as pages 1-124.

REMARKS

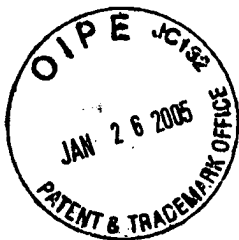
Applicants submit this substitute Sequence Listing to provide as a separate part of the disclosure, a "Sequence Listing" pursuant to 37 C.F.R §§1.821-1.825. In addition, Applicants submit herewith the substitute Sequence Listing in paper copy and on floppy disk in computer readable form. Applicants' amendments do not introduce new matter.

Dated: 1/24/05

By: 

David A. Casimir
Registration No. 42,395

MEDLEN & CARROLL, LLP
101 Howard Street, Suite 350
San Francisco, California 94105
415.904.6500



PATENT
Attorney Docket No. FORS-04447

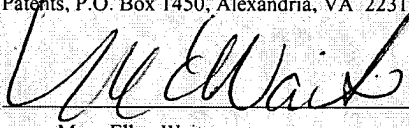
IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Michael W. Kaiser *et al.*
Serial No.: 09/684,305
Filed: 10/06/00
Entitled: IMPROVED CLEAVAGE AGENTS

Group No.: 1637
Examiner: JN Fredman

CERTIFICATE RE: SEQUENCE LISTING


MAIL STOP PETITION
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

CERTIFICATE OF MAILING UNDER 37 C.F.R. § 1.8(a)(1)(i)(A)	
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Dated: 1/24/05	By:  Mary Ellen Waite

Sir or Madam:

I hereby state that the enclosed Sequence Listing is being submitted in paper copy and on a computer-readable diskette, and that the content of the paper and computer readable copies are the same.

Dated: 1/24/05

By: 

David A. Casimir
Registration No. 42,395

MEDLEN & CARROLL, LLP
101 Howard Street, Suite 350
San Francisco, California 94105
415.904.6500



SEQUENCE LISTING

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 Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys
 115 120 125
 Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp
 130 135 140
 Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly
 145 150 155 160
 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
 165 170 175
 Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn
 180 185 190
 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu
 195 200 205
 Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu
 210 215 220
 Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys
 225 230 235 240
 Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val
 245 250 255
 Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe
 260 265 270
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285
 Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp
 305 310 315 320
 Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro
 325 330 335
 Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu
 405 410 415

Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu
 420 425 430
 Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala
 450 455 460
 Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr
 530 535 540
 Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu
 545 550 555 560
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590
 Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala
 595 600 605
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
 625 630 635 640
 Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro
 645 650 655
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
 660 665 670
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685
 Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 690 695 700
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
 705 710 715 720
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg
 725 730 735
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 740 745 750

Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
755 760 765

Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His
770 775 780

Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala
785 790 795 800

Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
805 810 815

Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu
820 825 830

<210> 5
<211> 831
<212> PRT
<213> thermus flavus

<400> 5
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Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys
35 40 45

Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Val Val Val Val Val
50 55 60

Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala Tyr
65 70 75 80

Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu Ala
85 90 95

Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Val Arg Leu Glu Val
100 105 110

Pro Gly Phe Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Arg Ala
115 120 125

Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp Leu
130 135 140

Tyr Gln Leu Leu Ser Glu Arg Ile Ala Ile Leu His Pro Glu Gly Tyr
145 150 155 160

Leu Ile Thr Pro Ala Trp Leu Tyr Glu Lys Tyr Gly Leu Arg Pro Glu
165 170 175

Gln Trp Val Asp Tyr Arg Ala Leu Ala Gly Asp Pro Ser Asp Asn Ile
180 185 190

Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Gln Arg Leu Ile Arg
 195 200 205
 Glu Trp Gly Ser Leu Glu Asn Leu Phe Gln His Leu Asp Gln Val Lys
 210 215 220
 Pro Ser Leu Arg Glu Lys Leu Gln Ala Gly Met Glu Ala Leu Ala Leu
 225 230 235 240
 Ser Arg Lys Leu Ser Gln Val His Thr Asp Leu Pro Leu Glu Val Asp
 245 250 255
 Phe Gly Arg Arg Arg Thr Pro Asn Leu Glu Gly Leu Arg Ala Phe Leu
 260 265 270
 Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu Glu
 275 280 285
 Gly Pro Lys Ala Ala Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly Ala
 290 295 300
 Phe Leu Gly Phe Ser Phe Ser Arg Pro Glu Pro Met Trp Ala Glu Leu
 305 310 315 320
 Leu Ala Leu Ala Gly Ala Trp Glu Gly Arg Leu His Arg Ala Gln Asp
 325 330 335
 Pro Leu Arg Gly Leu Arg Asp Leu Lys Gly Val Arg Gly Ile Leu Ala
 340 345 350
 Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Phe Pro
 355 360 365
 Glu Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn Thr
 370 375 380
 Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu Asp
 385 390 395 400
 Ala Gly Glu Arg Ala Leu Leu Ala Glu Arg Leu Phe Gln Thr Leu Lys
 405 410 415
 Glu Arg Leu Lys Gly Glu Glu Arg Leu Leu Trp Leu Tyr Glu Glu Val
 420 425 430
 Glu Lys Pro Leu Ser Arg Val Leu Ala Arg Met Glu Ala Thr Gly Val
 435 440 445
 Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Glu Ala
 450 455 460
 Glu Val Arg Gln Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His Pro
 465 470 475 480
 Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp Glu
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 Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile Val
 515 520 525

<210> 6
 <211> 834
 <212> PRT
 <213> Thermus thermophilus

<400> 6
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 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
 35 40 45
 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Tyr Lys Ala Val Phe
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu
 65 70 75 80
 Ala Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Phe Thr Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Val Leu Ala Thr Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg
 130 135 140
 Asp Leu Tyr Gln Leu Val Ser Asp Arg Val Ala Val Leu His Pro Glu
 145 150 155 160
 Gly His Leu Ile Thr Pro Glu Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Glu Gln Trp Val Asp Phe Arg Ala Leu Val Gly Asp Pro Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Leu Lys Leu
 195 200 205
 Leu Lys Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Val Lys Pro Glu Asn Val Arg Glu Lys Ile Lys Ala His Leu Glu Asp
 225 230 235 240
 Leu Arg Leu Ser Leu Glu Leu Ser Arg Val Arg Thr Asp Leu Pro Leu
 245 250 255
 Glu Val Asp Leu Ala Gln Gly Arg Glu Pro Asp Arg Glu Gly Leu Arg
 260 265 270
 Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
 275 280 285
 Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300

Glu 305	Gly	Ala	Phe	Val	Gly 310	Phe	Val	Leu	Ser	Arg 315	Pro	Glu	Pro	Met	Trp 320
Ala	Glu	Leu	Lys	Ala 325	Leu	Ala	Ala	Cys	Arg 330	Asp	Gly	Arg	Val	His 335	Arg
Ala	Ala	Asp	Pro 340	Leu	Ala	Gly	Leu	Lys 345	Asp	Leu	Lys	Glu	Val 350	Arg	Gly
Leu	Leu	Ala 355	Lys	Asp	Leu	Ala	Val 360	Leu	Ala	Ser	Arg	Glu 365	Gly	Leu	Asp
Leu	Val 370	Pro	Gly	Asp	Asp	Pro	Met 375	Leu	Leu	Ala	Tyr 380	Leu	Leu	Asp	Pro
Ser 385	Asn	Thr	Thr	Pro	Glu 390	Gly	Val	Ala	Arg	Arg 395	Tyr	Gly	Gly	Glu	Trp 400
Thr	Glu	Asp	Ala	Ala 405	His	Arg	Ala	Leu	Leu 410	Ser	Glu	Arg	Leu	His 415	Arg
Asn	Leu	Leu	Lys 420	Arg	Leu	Glu	Gly	Glu 425	Glu	Lys	Leu	Leu	Trp 430	Leu	Tyr
His	Glu	Val 435	Glu	Lys	Pro	Leu	Ser 440	Arg	Val	Leu	Ala	His 445	Met	Glu	Ala
Thr	Gly 450	Val	Arg	Leu	Asp	Val 455	Ala	Tyr	Leu	Gln	Ala 460	Leu	Ser	Leu	Glu
Leu 465	Ala	Glu	Glu	Ile	Arg 470	Arg	Leu	Glu	Glu	Glu 475	Val	Phe	Arg	Leu	Ala 480
Gly	His	Pro	Phe	Asn 485	Leu	Asn	Ser	Arg	Asp 490	Gln	Leu	Glu	Arg	Val 495	Leu
Phe	Asp	Glu	Leu 500	Arg	Leu	Pro	Ala	Leu 505	Gly	Lys	Thr	Gln	Lys 510	Thr	Gly
Lys	Arg	Ser 515	Thr	Ser	Ala	Ala	Val 520	Leu	Glu	Ala	Leu	Arg 525	Glu	Ala	His
Pro 530	Ile	Val	Glu	Lys	Ile	Leu 535	Gln	His	Arg	Glu	Leu 540	Thr	Lys	Leu	Lys
Asn 545	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val 555	His	Pro	Arg	Thr	Gly 560
Arg	Leu	His	Thr	Arg 565	Phe	Asn	Gln	Thr	Ala 570	Thr	Ala	Thr	Gly	Arg 575	Leu
Ser	Ser	Ser	Asp 580	Pro	Asn	Leu	Gln	Asn 585	Ile	Pro	Val	Arg	Thr 590	Pro	Leu
Gly	Gln	Arg 595	Ile	Arg	Arg	Ala	Phe 600	Val	Ala	Glu	Ala	Gly 605	Trp	Ala	Leu
Val 610	Ala	Leu	Asp	Tyr	Ser	Gln 615	Ile	Glu	Leu	Arg	Val 620	Leu	Ala	His	Leu
Ser 625	Gly	Asp	Glu	Asn	Leu 630	Ile	Arg	Val	Phe	Gln 635	Glu	Gly	Lys	Asp	Ile 640

His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
 820 825 830
 Lys Gly

<210> 7
 <211> 2502
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

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<220>
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 <222> (181)..(182)
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<220>
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 <222> (366)
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 <221> misc_feature
 <222> (617)
 <223> The n at this position can be a, c, t or g.

<220>
 <221> misc_feature
 <222> (628)
 <223> The n at this position can be a, c, t or g.

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 <221> misc_feature
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 <223> The n a this position can be a, c, t or g.

<220>
 <221> misc_feature
 <222> (714)
 <223> The n at this position can be a, c, t or g.

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<220>
 <221> misc_feature
 <222> (784)
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 <222> (1022)
 <223> The n at this position can be a, c, t or g.

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 <221> misc_feature
 <222> (1029)
 <223> The n at this position can be a, c, t or g.

<220>
 <221> misc_feature
 <222> (1038)
 <223> The n at this position can be a, c, t or g.

<220>
 <221> misc_feature
 <222> (1053)
 <223> The n at this position can be a, c, t or g.

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 <221> misc_feature
 <222> (1098)
 <223> The n at this position can be a, c, t or g.

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 <221> misc_feature
 <222> (1105)
 <223> The n at this position can be a, c, t or g.

<220>
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 <222> (1206)
 <223> The n at this position can be a, c, t or g.

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 <221> misc_feature
 <222> (1227)
 <223> The n at this position can be a, c, t or g.

<220>
 <221> misc_feature
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 <223> The n at this position can be a, c, t or g.

<220>
 <221> misc_feature
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 <223> The n at these positions can be a, c, t or g.

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 <223> The n at this position can be a, c, t or g.

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 <221> misc_feature
 <222> (1380)
 <223> The n at this position can be a, c, t or g.

<220>
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 <222> (1497)
 <223> The n at this positon can be a, c, t or g.

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 <222> (1530)
 <223> The n at this position can be a, c, t or g.

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 <222> (1569)
 <223> The n at this position can be a, c, t or g.

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 <222> (1653)
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 <222> (1770)
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 <222> (1812)
 <223> The n at this position can be a, c, t or g.

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 <221> misc_feature
 <222> (2319)
 <223> The n at this position can be a, c, t or g.

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 <221> misc_feature
 <222> (2346)
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<220>
 <221> misc_feature
 <222> (2396)
 <223> The n at this position can be a, c, t or g.

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 gtgcaggcgg tctacggctt cgccaagagc ctctcaagg ccctgaagga ggacggggac 180
 nnggcggtgn tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacgag 240
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 aaggagctgg tggacctcct ggggcttgcg cgcctcgagg tcccggcta cgaggcggac 360
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 ccccgccgg aaggggcctt cgtgggcttt gtcctttccc gccccgagcc catgtgggcc 960
 gagcttctgg ccctggccgc cgccaggag ggccgggtcc accgggcacc agacccttt 1020
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 gccctgaggg agggcctnga cctcntgccc ggggacgacc ccattgctcct cgcctacctc 1140
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 gaggangcgg gggagcgggc cctcctntcc gagaggctct tcngaacct nngcagcgc 1260
 cttgaggggg aggagaggct cctttggctt taccaggagg tggagaagcc cttttcccg 1320
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 cttcccgcca tcggcaagac ggagaagacn ggcaagcgt ccaccagcgc cgccgtgctg 1560
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 aagctcaaga acacctacat ngacccctg ccngncctcg tccacccag gacgggccgc 1680
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 aacctgcaga acatccccgt ccgcacccn ctgggcccaga ggatccgccg ggccttcgtg 1800
 gccgaggagg gntgggtgtt ggtggccctg gactatagcc agatagagct ccgggtcctg 1860
 gccacctct ccggggacga gaacctgatc cgggtcttcc aggaggggag ggacatccac 1920
 acccagaccg ccagctggat gttcggcgtc ccccgaggag ccgtggaccc cctgatgcgc 1980
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 gtggagacct tcttcggccg ccggcgctac gtgcccagcc tcaacgcccg ggtgaagagc 2220
 gtgcgggagg cggcgaggcg catggccttc aacatgcccg tccagggcac cgccgccgac 2280
 ctcatgaagc tggccatggt gaagctcttc ccccggtnc aggaaatggg ggccaggatg 2340
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 gaggtgggga tgggggagga ctggctctcc gccaaaggag ag 2502

<210> 8
 <211> 833
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

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 <222> (2)
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 <220>
 <221> SITE
 <222> (63)
 <223> Xaa at this position can be any amino acid.

 <220>
 <221> SITE
 <222> (109)
 <223> Xaa at this position can be any amino acid.

 <220>
 <221> SITE
 <222> (186)
 <223> Xaa at this position can be any amino acid.

 <220>
 <221> SITE
 <222> (205)
 <223> Xaa at this position can be any amino acid.

 <220>
 <221> SITE
 <222> (209)
 <223> Xaa at this position can be any amino acid.

 <220>
 <221> SITE
 <222> (227)..(228)
 <223> Xaa at these positions can be any amino acid.

 <220>
 <221> SITE
 <222> (233)
 <223> Xaa at this position can be any amino acid.

 <220>
 <221> SITE
 <222> (240)
 <223> Xaa at this position can be any amino acid.

 <220>
 <221> SITE
 <222> (243)..(244)
 <223> Xaa at these positions can be any amino acid.

 <220>
 <221> SITE
 <222> (247)
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<220>
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 <223> Xaa at this position can be any amino acid.

<220>
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 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (329)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (336)
 <223> Xaa at this position can be any amino acid.

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 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (368)
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<220>
 <221> SITE
 <222> (414)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (417) .. (418)
 <223> Xaa at these positions can be any amino acid.

<220>
 <221> SITE
 <222> (431)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (551)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (605)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (773)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (794)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (798)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (823)
 <223> Xaa at this position can be any amino acid.

<220>
 <221> SITE
 <222> (833)
 <223> Xaa at this position can be any amino acid.

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 Val Asp Gly His His Leu Ala Tyr Arg Thr Phe Phe Ala Leu Lys Gly
 20 25 30
 Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala
 35 40 45
 Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Xaa Val
 50 55 60
 Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Glu Ala
 65 70 75 80
 Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu
 85 90 95
 Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Xaa Arg Leu Glu
 100 105 110
 Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Thr Leu Ala Lys Lys
 115 120 125
 Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Arg Asp
 130 135 140
 Leu Tyr Gln Leu Leu Ser Asp Arg Ile Ala Val Leu His Pro Glu Gly
 145 150 155 160
 Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro
 165 170 175
 Glu Gln Trp Val Asp Tyr Arg Ala Leu Xaa Gly Asp Pro Ser Asp Asn
 180 185 190
 Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Xaa Lys Leu Leu
 195 200 205
 Xaa Glu Trp Gly Ser Leu Glu Asn Leu Leu Lys Asn Leu Asp Arg Val
 210 215 220

Lys Pro Xaa Xaa Arg Glu Lys Ile Xaa Ala His Met Glu Asp Leu Xaa
 225 230 235 240
 Leu Ser Xaa Xaa Leu Ser Xaa Val Arg Thr Asp Leu Pro Leu Glu Val
 245 250 255
 Asp Phe Ala Xaa Arg Arg Glu Pro Asp Arg Glu Gly Leu Arg Ala Phe
 260 265 270
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285
 Glu Xaa Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp Ala Glu
 305 310 315 320
 Leu Leu Ala Leu Ala Ala Ala Arg Xaa Gly Arg Val His Arg Ala Xaa
 325 330 335
 Asp Pro Leu Xaa Gly Leu Arg Asp Leu Lys Glu Val Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ala Val Leu Ala Leu Arg Glu Gly Leu Asp Leu Xaa
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Asp Ala Gly Glu Arg Ala Leu Leu Ser Glu Arg Leu Phe Xaa Asn Leu
 405 410 415
 Xaa Xaa Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Xaa Glu
 420 425 430
 Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Leu Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu Val Ala
 450 455 460
 Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Asn Thr
 530 535 540
 Tyr Ile Asp Pro Leu Pro Xaa Leu Val His Pro Arg Thr Gly Arg Leu
 545 550 555 560

His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590
 Arg Ile Arg Arg Ala Phe Val Ala Glu Glu Gly Trp Xaa Leu Val Ala
 595 600 605
 Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
 625 630 635 640
 Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val Asp Pro
 645 650 655
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
 660 665 670
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685
 Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 690 695 700
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
 705 710 715 720
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn Ala Arg
 725 730 735
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 740 745 750
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
 755 760 765
 Phe Pro Arg Leu Xaa Glu Met Gly Ala Arg Met Leu Leu Gln Val His
 770 775 780
 Asp Glu Leu Val Leu Glu Ala Pro Lys Xaa Arg Ala Glu Xaa Val Ala
 785 790 795 800
 Ala Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
 805 810 815
 Leu Glu Val Glu Val Gly Xaa Gly Glu Asp Trp Leu Ser Ala Lys Glu
 820 825 830

Xaa

<210> 9

<211> 1647

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 9
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caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggcccggc cccacgcgcg gaggactttc cccggcaact cgcctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggctttgg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccatat ggacgatctg 720
aagctctcct gggacctggc caagggtgcg accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagagggt tgagtttggc 840
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gccctgaggg aaggccttgg cctcccgcgc ggcgacgacc ccattgctcct cgcctacctc 1140
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tccttgaggg tggccgggga gatcgcgcgc ctcgaggccg aggtcttccg cctggccggc 1440
cacccttca acctcaactc cggggaccag ctggaaaagg tcctctttga cgagctaggg 1500
cttcccgcga tcggcaagac ggagaagacc ggcaagcgct ccaccagcgc cgccgtcctg 1560
gaggccctcc gcgaggccca ccccatcgtg gagaagatcc tgcaggcatg caagcttggc 1620
actggccgtc gttttacaac gtcgtga 1647

<210> 10
<211> 2088
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 10

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ccggtgcagg cggctctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggccgggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420
accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggg caagggcac 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc ctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
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gccctgaggg aaggccttgg cctcccgcgc ggcgacgacc ccatgctcct cgcctacctc 1140
ctggaccctt ccaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200
gaggaggcgg gggagcgggc cgccctttcc gagaggctct tcgccaacct gtggggggagg 1260
cttgaggggg aggagaggct ctttggtt taccgggagg tggagaggcc cttttccgct 1320
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cttcccgcga tcggcaagac ggagaagacc ggcaagcgtc ccaccagcgc cgccgtcctg 1560
gaggccctcc gcgaggccca ccccatcggt gagaagatcc tgcagtaccg ggagctcacc 1620
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aagctgaaga gcacctacat tgaccccttg ccggacctca tccaccccag gacggggccgc 1680
ctccacaccc gcttcaacca gacggccacg gccacgggca ggctaagtag ctccgatccc 1740
aacctccaga acatccccgt ccgcaccccg cttgggcaga ggatccgccg ggccttcac 1800
gccgaggagg ggtggctatt ggtggccctg gactatagcc agatagagct cagggtgctg 1860
gcccacctct ccggcgacga gaacctgatc cgggtcttcc aggaggggcg ggacatccac 1920
acggagaccg ccagctggat gttcggcgtc ccccgggagg ccgtggaccc cctgatgcgc 1980
cgggcggcca agaccatcaa cttcggggtc ctctacggca tgcggccca ccgcctctcc 2040
caggagctag ctagccatcc cttacgagga ggcccaggcc ttcattga 2088

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<210> 11

<211> 962

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 11

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atgaattcgg ggatgctgcc cctctttgag cccaagggcc gggtcctcct ggtggacggc 60
caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
ccggtgcagg cggcttacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
gggtacaagg cgggcccggc cccacgcgcg gaggactttc cccggcaact cgccctcatc 300
aaggagctgg tggacctcct ggggctggcg cgcctcgagg tcccgggcta cgaggcggac 360
gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcctcctc 420
accgccgaca aagaccttta ccagcttctt tccgaccgca tccacgtcct ccaccccgag 480
gggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540
gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcac 600
ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
aagctctcct gggacctggc caaggtgcgc accgacctgc ccctggaggt ggacttcgcc 780
aaaaggcggg agcccgaccg ggagaggctt agggcctttc tggagaggct tgagtttggc 840
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ga 962

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<210> 12
 <211> 1600
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 12

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ccaccacctg gcctaccgca ccttccacgc cctgaagggc ctcaccacca gccgggggga 120
gccggtgcag gcggtctacg gcttcgcca gagcctctc aaggccctca aggaggacgg 180
ggacgcggtg atcgtggtct ttgacgcca gggccctcc ttccgccacg aggcctacgg 240
ggggtacaag gcgggcccgg ccccccacgc ggaggacttt ccccggaac tcgccctcat 300
caaggagctg gtggacctcc tggggctggc gcgcctcgag gtcccgggct acgaggcgga 360
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caccgccgac aaagaccttt accagctcct ttccgaccgc atccacgtcc tccaccccga 480
ggggtacctc atcaccccg cctggctttg ggaaaagtac ggctgaggc ccgaccagt 540
ggccgactac cgggccctga cgggggacga gtccgacaac cttcccgggg tcaagggcat 600
cggggagaag acggcgagga agcttctgga ggagtggggg agcctggaag ccctcctcaa 660
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caaaaggcgg gagcccgacc gggagaggct tagggccttt ctggagaggc ttgagtttgg 840
cagcctctc cagcagttcg gccttctgga aagccccaag atccgccggg ccttcctcgc 900
cgaggagggg tggctattgg tggccctgga ctatagccag atagagctca gggtgctggc 960
ccacctctcc ggcgacgaga acctgatccg ggtcttccag gagggcgggg acatccacac 1020
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ccttcaggtc cagcagcagc tggctctcga gggcccaaaa gagagggcgg aggccgtggc 1500
ccggctggcc aaggaggtca tggagggggg gtatcccctg gccgtgcccc tggaggtgga 1560
ggtggggata ggggaggact ggctctccgc caaggagtga 1600

```

<210> 13
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 13
 cacgaattcg gggatgctgc ccctctttga gcccaa 36

 <210> 14
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 14
 gtgagatcta tcactccttg gcggagagcc agtc 34

 <210> 15
 <211> 91
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 15
 taatacgact cactataggg agaccggaat tcgagctcgc ccgggcgagc tcgaattccg 60
 tgtattctat agtgtcacct aaatcgaatt c 91

 <210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 16
 taatacgact cactataggg 20

 <210> 17
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 17
 gaattcgatt taggtgacac tatagaa 27

<210> 18
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 18
 gtaatcatgg tcatagctgg tagcttgcta c 31

 <210> 19
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 19
 ggatcctcta gagtcgacct gcaggcatgc ctaccttggg ag 42

 <210> 20
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 20
 ggatcctcta gagtcgacct gcaggcatgc 30

 <210> 21
 <211> 2502
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 21
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 caccacctgg cctaccgcac cttccacgcc ctgaagggcc tcaccaccag ccgggggggag 120
 ccggtgcagg cgggtctacgg cttcgccaag agcctcctca aggccctcaa ggaggacggg 180
 gacgcggtga tcgtggtctt tgacgccaag gccccctcct tccgccacga ggcctacggg 240
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 aaggagctgg tggacctcct ggggctggcg cgctcgagg tcccgggcta cgaggcggac 360
 gacgtcctgg ccagcctggc caagaaggcg gaaaaggagg gctacgaggt ccgcatcctc 420
 accgccgaca aagaccttta ccagctcctt tccgaccgca tccacgtcct ccaccccgag 480
 ggggtacctca tcaccccggc ctggcttttg gaaaagtacg gcctgaggcc cgaccagtgg 540

gccgactacc gggccctgac cggggacgag tccgacaacc ttcccggggt caagggcatc 600
 ggggagaaga cggcgaggaa gcttctggag gagtggggga gcctggaagc cctcctcaag 660
 aacctggacc ggctgaagcc cgccatccgg gagaagatcc tggcccacat ggacgatctg 720
 aagctctcct gggacctggc caaggtgcg cccgacctgc ccctggaggt ggacttcgcc 780
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 ccccgccgg aaggggcctt cgtgggcttt gtgctttccc gcaaggagcc catgtgggcc 960
 gatcttctgg ccctggccgc cgccaggggg ggccgggtcc accgggcccc cgagccttat 1020
 aaagccctca gggacctgaa ggaggcgcg gggcttctcg ccaaagacct gagcgttctg 1080
 gccctgaggg aaggccttgg cctcccgccc ggcgacgacc ccatgctcct cgcctacctc 1140
 ctggaccctt ccaacaccac ccccgagggg gtggcccggc gctacggcgg ggagtggacg 1200
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 cttgaggggg aggagaggct cctttggctt taccgggagg tggagaggcc cctttccgct 1320
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 cttcccgcca tcggcaagac ggagaagacc ggcaagcgt ccaccagcgc cgccgtcctg 1560
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 ctccttcagg tccacgacga gctggctctc gaggcccaa aagagagggc ggaggccgtg 2400

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gaggtgggga taggggagga ctggctctcc gccaaaggagt ga 2502

<210> 22
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 22
gatttaggtg acactatag 19

<210> 23
<211> 72
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 23
cggacgaaca agcgagacag cgacacaggt accacatggt acaagaggca agagagacga 60
cacagcagaa ac 72

<210> 24
<211> 70
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 24
gtttctgctg tgctgtctct cttgcctctt gtaccatgtg gtacctgtgt cgctgtctcg 60
cttgttcgtc 70

<210> 25
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 25
gacgaacaag cgagacagcg 20

<210> 26
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 26
 gtttctgctg tgctgtctct cttg 24

<210> 27
 <211> 46
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 27
 cctctgttac catgtggtac ctgtgtcgtc gtctcgcttg ttcgtc 46

<210> 28
 <211> 50
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 28
 acacaggtac cacatggtac aagaggcaag agagacgaca cagcagaaac 50

<210> 29
 <211> 15
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 29
 Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser
 1 5 10 15

<210> 30
 <211> 969
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 30
 atggctagca tgactggtgg acagcaaatg ggtcggatca attcggggat gctgcccctc 60
 tttgagccca agggccgggt cctcctggtg gacggccacc acctggccta ccgcaccttc 120

cacgccctga agggcctcac caccagccgg ggggagccgg tgcaggcgggt ctacggcttc 180
 gccaagagcc tcctcaaggc cctcaaggag gacggggacg cggatgatcgt ggtctttgac 240
 gccaaggccc cctccttcg ccacgaggcc tacgggggggt acaaggcggg ccgggcccc 300
 acgccggagg actttccccg gcaactcgcc ctcatcaagg agctggtgga cctcctgggg 360
 ctggcgcgcc tcgaggtccc gggctacgag gcggacgacg tcctggccag cctggccaag 420
 aaggcggaaa aggagggcta cgaggtccgc atcctcaccg ccgacaaaga cctttaccag 480
 cttcttttcg accgcatcca cgtcctccac cccgaggggt acctcatcac cccggcctgg 540
 ctttgggaaa agtacggcct gaggcccgac cagtgggccc actaccgggc cctgaccggg 600
 gacgagtccg acaaccttcc cggggtcaag ggcacgggg agaagacggc gaggaagctt 660
 ctggaggagt gggggagcct ggaagccctc ctcaagaacc tggaccgggt gaagcccgcc 720
 atccgggaga agatcctggc ccacatggac gatctgaagc tctcctggga cctggccaag 780
 gtgcgacccg acctgcccct ggaggtggac ttgcgcaaaa ggcgggagcc cgaccgggag 840
 aggccttaggg cctttctgga gaggttgag tttggcagcc tcctccacga gttcggcctt 900
 ctggaaagcc ccaagtcag gagggggtgt atccctggc cgtgcccctg gaggtggagg 960
 tggggatag 969

<210> 31

<211> 948

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 31

atggctagca tgactggtgg acagcaaatg ggtcggatca attcggggat gctgcccctc 60
 tttgagccca agggccgggt cctcctggtg gacggccacc acctggccta ccgcaccttc 120
 cacgccctga agggcctcac caccagccgg ggggagccgg tgcaggcgggt ctacggcttc 180
 gccaagagcc tcctcaaggc cctcaaggag gacggggacg cggatgatcgt ggtctttgac 240
 gccaaggccc cctccttcg ccacgaggcc tacgggggggt acaaggcggg ccgggcccc 300
 acgccggagg actttccccg gcaactcgcc ctcatcaagg agctggtgga cctcctgggg 360
 ctggcgcgcc tcgaggtccc gggctacgag gcggacgacg tcctggccag cctggccaag 420
 aaggcggaaa aggagggcta cgaggtccgc atcctcaccg ccgacaaaga cctttaccag 480
 cttcttttcg accgcatcca cgtcctccac cccgaggggt acctcatcac cccggcctgg 540
 ctttgggaaa agtacggcct gaggcccgac cagtgggccc actaccgggc cctgaccggg 600
 gacgagtccg acaaccttcc cggggtcaag ggcacgggg agaagacggc gaggaagctt 660

ctggaggagt gggggagcct ggaagccctc ctcaagaacc tggaccggct gaagcccgcc 720
atccgggaga agatcctggc ccacatggac gatctgaagc tctcctggga cctggccaag 780
gtgcgacccg acctgcccct ggaggtggac ttcgccaaaa ggcgggagcc cgaccgggag 840
aggcttaggg cctttctgga gaggttgag tttggcagcc tcctccacga gttcggcctt 900
ctggaaagcc ccaaggccgc actcgagcac caccaccacc accactga 948

<210> 32
<211> 206
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 32
cgccagggtt ttcccagtcg cgacgttgta aaacgacggc cagtgaattg taatacgact 60
cactataggg cgaattcgag ctcggtaccc ggggatcctc tagagtcgac ctgcaggcat 120
gcaagcttga gtattctata gtgtcaccta aatagcttgg cgtaatcatg gtcatagctg 180
tttctgtgtg gaaattgtta tccgct 206

<210> 33
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 33
ttctgggttc tctgctctct ggctcgctgc tcgcttggtc gtc 43

<210> 34
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 34
gctgtctcgc ttgttcgctc 19

<210> 35
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 35
 gacgaacaag cgagacagcg 20

<210> 36
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 36
 ttctgggttc tctgctctct ggtc 24

<210> 37
 <211> 43
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 37
 gacgaacaag cgagacagcg accagagagc agagaaccca gaa 43

<210> 38
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 38
 accagagagc agagaaccca gaa 23

<210> 39
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 39
 aacagctatg accatgatta c 21

<210> 40
 <211> 60
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 40
 gttctctgct ctctggctgc tgtctcgctt gtgaaacaag cgagacagcg tggctctctcg 60

<210> 41
 <211> 15
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 41
 cgagagacca cgctg 15

 <210> 42
 <211> 52
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 42
 cctttcgctt tcttccttc ctttctcgcc acgttcgccg gctttccccg tc 52

 <210> 43
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 43
 agaaaggaag ggaagaaagc gaaagg 26

 <210> 44
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 44
 gacggggaaa gccggcgaac g 21

 <210> 45
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 45
 gaaagccggc gaacgtggcg 20

<210> 46
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 46
 ggcgaacgtg gcgagaaagg a 21

 <210> 47
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 47
 cctttcgctt tcttcccttc ctttctcgcc acgttcgccg gc 42

 <210> 48
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 48
 cctttcgctc tcttcccttc ctttctcgcc acgttcgccg gc 42

 <210> 49
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <222> (8)
 <223> The A residue at this position is
 2'-O-methyladenosine.

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 49
 agaaaggaag ggaagaaagc gaaaggt 27

 <210> 50
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

<400> 50 gccggcgaac gtggcgagaa agga	24
<210> 51 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic	
<400> 51 ggtttttctt tgaggtttag	20
<210> 52 <211> 19 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic	
<400> 52 gcgacactcc accatagat	19
<210> 53 <211> 19 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic	
<400> 53 ctgtcttcac gcagaaagc	19
<210> 54 <211> 19 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic	
<400> 54 gcacggtcta cgagacctc	19
<210> 55 <211> 20 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Synthetic	
<400> 55 taatacgact cactataggg	20

<210> 56
<211> 337
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 56
gggaaagcuu gcaugccugc agguccgacuc uagaggaucau acuagucaua uggauucugu 60
cuucacgcag aaagcgucug gccauggcgu uaguaugagu gucgugcagc cuccaggacc 120
ccccucuccg ggagaggcau aguggucugc ggaaccggug aguacaccgg aaugccagg 180
acgaccgggu ccuuucuugg auaaaccgc ucaaugccug gagauuuggg cgugcccccg 240
caagacugcu agccgaguag uguugggucg cgaaaggccu ugugguacug ccugauaggg 300
ugccugcgag ugccccggga ggucucguag accgugc 337

<210> 57
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<220>
<221> misc_feature
<222> (17)
<223> The T at this position is linked to a fluorescein
dye on an abasic linker.

<400> 57
ccggtcgtcc tggcaatcc 19

<210> 58
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 58
gtttatccaa gaaaggaccc ggtc 24

<210> 59
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 59
 cagggtgaag ggaagaagaa agcgaaaggt 30

<210> 60
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 60
 cagggggaag ggaagaagaa agcgaaaggt 30

<210> 61
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)..(2)
 <223> The T residues at positions 1 and 2 are amino modified T residues.

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 61
 ttcttttcac cagcgagacg gg 22

<210> 62
 <211> 22
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 62
 attgggcgcc aggggtggttt tt 22

<210> 63
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 63
 cccgtctcgc tggtgaaaag aaaaaccacc ctggcgccca atacgcaaac cgc 53

<210> 64
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 64
 gaattcgatt taggtgacac tatagaatac a 31

<210> 65
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 65
 cctttcgctt tcttcccttc ctttctcgcc acgttcgccg gc 42

<210> 66
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 66
 gccggcgaac gtggcgagaa agga 24

<210> 67
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 67
 cagaaggaag ggaagaaagc gaaagg 26

<210> 68
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 68
 cagggggaag ggaagaaagc gaaagg 26

<210> 69
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 69
 cagggtacag ggaagaaagc gaaagg 26

 <210> 70
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <222> (24)
 <223> The residue at this position is a dideoxycytidine.

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 70
 gccggcgaac gtggcgagaa aggc 24

 <210> 71
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <220>
 <221> misc_feature
 <222> (26)
 <223> The G at this position is linked to a spacer
 bearing a Cy3 amidite group.

 <220>
 <221> misc_feature
 <222> (27)
 <223> The residue at this position is a dideoxycytidine.

 <400> 71
 agaaaggaag ggaagaaagc gaaaggc 27

 <210> 72
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <222> (1)
 <223> The A at this position is linked to a spacer
 containing a fluorescein label.

<220>
 <221> misc_feature
 <222> (26)
 <223> The G at this position is linked to a spacer
 bearing a Cy3 amidite group.

 <220>
 <221> misc_feature
 <222> (27)
 <223> The residue at this position is a dideoxycytidine.

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 72
 agaaaggaag ggaagaaagc gaaaggc 27

 <210> 73
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <222> (1)
 <223> The A at this position is linked to a spacer
 containing a fluorescein label.

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 73
 agaaaggaag ggaagaaagc gaaagg 26

 <210> 74
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <222> (1)
 <223> The A at this position is linked to a spacer
 bearing a Cy3 amidite group.

 <220>
 <221> misc_feature
 <222> (26)
 <223> The G at this position is linked to a spacer
 bearing a biotin group.

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 74
 agaaaggaag ggaagaaagc gaaaggt 27

<210> 75
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 75
 ggaaagccgg cgaacgtggc gaga 24

<210> 76
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 76
 ggaaagccgg cgaacgtggc gagaaa 26

<210> 77
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <222> (1)
 <223> The T at this position is linked to a spacer
 bearing a Cy3 amidite group.

 <220>
 <221> misc_feature
 <222> (1)..(2)
 <223> The residues at these positions have an amino
 group added.

 <220>
 <221> misc_feature
 <222> (22)
 <223> The T at this position is linked to a spacer
 containing a fluorescein label.

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 77
 ttccagagcc taatttgcca gta 23

<210> 78
 <211> 23
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)
 <223> The residue at this position has a 5' TET-label.

 <220>
 <221> misc_feature
 <222> (22)
 <223> The T at this position is linked to a spacer
 containing a fluorescein label.

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 78
 ttccagagcc taatttgcca gta 23

 <210> 79
 <211> 25
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 79
 cttaccaacg ctaacgagcg tcttg 25

 <210> 80
 <211> 14
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <222> (14)
 <223> The residue at this positions contain an abasic
 ribose.

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 80
 cgagagacca cgct 14

 <210> 81
 <211> 14
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <222> (14)
 <223> The residue at this position contains an abasic
 ribose with a 3' phosphate group.

 <220>
 <223> Description of Artificial Sequence: Synthetic

<400> 81
cgagagacca cgct 14

<210> 82
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (15)
<223> The residue at this position contains a 3'
phosphate group.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 82
cgagagacca cgctg 15

<210> 83
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 83
cccgtctcgc tgggtgaaaag aaaaaccacc ctggcgccca.ata 43

<210> 84
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (15)
<223> The G at this position is linked to a
3-nitropyrrole.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 84
tattgggcgc cagggggttt tt 22

<210> 85
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (15)
<223> The G at this position is linked to a
3-nitropyrrole group.

<220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 85
 tattgggcgc catggggttt tt 22

 <210> 86
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 86
 tattgggcgc catggtgggtt ttt 23

 <210> 87
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <222> (9)
 <223> The G at this position is linked to a
 5-nitroindole.

 <220>
 <221> misc_feature
 <222> (14)
 <223> The G at this position is linked to a
 5-nitroindole.

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 87
 tattgggcgc agggggtttt t 21

 <210> 88
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <222> (9)
 <223> The G at this position is linked to a
 5-nitroindole.

 <220>
 <221> misc_feature
 <222> (14)
 <223> The G at this position is linked to a
 5-nitroindole.

 <220>
 <223> Description of Artificial Sequence: Synthetic

<400> 88
tattgggcgc atgggggtttt t

21

<210> 89
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The T at this position is linked to a spacer
bearing a Cy3 amidite label.

<220>
<221> misc_feature
<222> (2)..(3)
<223> The residues at these positions have an amino
group added.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 89
ttcaccag

8

<210> 90
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The residue at this position is a 2'deoxyguanosine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (2)
<223> The residue at this position is a 2'deoxyctosine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (3)
<223> The residue at this position is a 2'deoxythymidine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (4)
<223> The residue at this position is a 2'deoxyctosine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (5)..(6)
<223> The residues at these positions are
2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (7)..(8)
 <223> The residues at these positions are
 2'deoxyguanosine 5'-O-(1-Thiomonophosphate)

 <220>
 <221> misc_feature
 <222> (9)
 <223> The residue at this position is a 2'deoxycytosine
 5'-O-(1-Thiomonophosphate).

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 90
 gctcaaggca ctcttgcccta cga

 <210> 91
 <211> 27
 <212> DNA
 <213> Artificial Sequence

 <220>
 <221> misc_feature
 <222> (1)
 <223> The residue at this position is a 2'deoxycytosine
 5'-O-(1-Thiomonophosphate).

 <220>
 <221> misc_feature
 <222> (2)
 <223> The residue at this position is a 2'deoxythymidine
 5'-O-(1-Thiomonophosphate).

 <220>
 <221> misc_feature
 <222> (3)..(4)
 <223> The residues at these positions are a
 2'deoxycytosine 5'-O-(1-Thiomonophosphate).

 <220>
 <221> misc_feature
 <222> (5)..(6)
 <223> The residues at these positions are a
 2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

 <220>
 <221> misc_feature
 <222> (7)
 <223> The residue at this position is a 2'deoxycytosine
 5'-O-(1-Thiomonophosphate).

 <220>
 <221> misc_feature
 <222> (8)
 <223> The residue at this position is a 2'deoxythymidine
 5'-O-(1-Thiomonophosphate).

23

<220>
<221> misc_feature
<222> (9)
<223> The residue at this position is a 2'deoxyadenosine
5'-O-(1-Thiomonophosphate).

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 91
ctccaactac cacaagttta tattcag

27

<210> 92
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The residue at this position is a 2'deoxycytosine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (2)
<223> The residue at this position is a 2'deoxythymidine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (3)
<223> The residue at this position is a 2'deoxyguanosine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (4)..(5)
<223> The residues at these positions are a
2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (6)
<223> The residue at this position is a 2'deoxythymidine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (7)
<223> The residue at this position is a 2'deoxyadenosine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (8)
<223> The residue at this position is a 2'deoxythymidine
5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (9)..(10)
 <223> The residues at these positions are a
 2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 92
 ctgaatataa acttgtggta gttggagctg gtgacgtagg caagagtgcc ttgacg 56

<210> 93
 <211> 56
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)
 <223> The residue at this position is a 2'deoxycytosine
 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (2)
 <223> The residue at this position is a 2'deoxythymidine
 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (3)
 <223> The residue at this position is a 2'deoxyguanosine
 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (4)..(5)
 <223> The residues at these positions are a
 2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (6)
 <223> The residue at this position is a 2'deoxythymidine
 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (7)
 <223> The residue at this position is a 2'deoxyadenosine
 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (8)
 <223> The residue at this position is a 2'deoxythymidine
 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (9)..(10)
 <223> The residues at these positions are a
 2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 93
 ctgaatataa acttgtggta gttggagctg gtgccgtagg caagagtgcc ttgacg 56

<210> 94
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)
 <223> The residue at this position has a TET label.

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 94
 ccggtcgtcc tggcaa 16

<210> 95
 <211> 13
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)
 <223> The residue at this position has a TET label.

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 95
 ccggtcgtcc tgg 13

<210> 96
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 96
 caattccggt gtactcaccg gttcc 25

<210> 97
<211> 8
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The T at this position is linked to a spacer
bearing a Cy3 amidite label.

<220>
<221> misc_feature
<222> (2)..(3)
<223> The residues at these positions have an amino
group added.

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 97
ttccagag

8

<210> 98
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)
<223> The residue at this position is a 2'deoxyguanosine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (2)
<223> The residue at this position is a 2'deoxythymidine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (3)..(4)
<223> The residues at these positions are a
2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (5)
<223> The residue at this position is a 2'deoxythymidine
5'-O-(1-Thiomonophosphate).

<220>
<221> misc_feature
<222> (6)
<223> The residue at this position is a 2'deoxycytosine
5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (7)..(8)
 <223> The residues at these positions are a
 2'deoxythymidine 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (9)
 <223> The residue at this position is a 2'deoxyadenosine
 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (10)
 <223> The residue at this position is a 2'deoxycytosine
 5'-O-(1-Thiomonophosphate).

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 98
 gtaatcttac caacgctaac gagcgtcttg

<210> 99
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> misc_feature
 <222> (1)..(2)
 <223> The residues at these positions are a
 2'deoxycytosine 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (3)
 <223> The residue at this position is a 2'deoxythymidine
 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (4)..(5)
 <223> The residues at these positions are a
 2'deoxyadenosine 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (6)..(8)
 <223> The residues at these positions are a
 2'deoxythymidine 5'-O-(1-Thiomonophosphate).

<220>
 <221> misc_feature
 <222> (9)
 <223> The residue at this position is a 2'deoxyguanosine
 5'-O-(1-Thiomonophosphate).

30

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<220>
<221> misc_feature
<222> (10)
<223> The residue at this position is a 2'deoxycytosine
      5'-O-(1-Thiomonophosphate).

<220>
<223> Description of Artificial Sequence:  Synthetic

<400> 99
cctaatttgc cagttacaaa ataaacagcc
                                         30

<210> 100
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic

<400> 100
gggaaagtcc tcggagccgc gcgggacgag cgtggggggcc cg
                                         42

<210> 101
<211> 963
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic

<220>
<221> CDS
<222> (1) .. (960)

<400> 101
atg gct agc atg act ggt gga cag caa atg ggt cgg atc aat tcg ggg 48
Met Ala Ser Met Thr Gly Gly Gln Gln Met Gly Arg Ile Asn Ser Gly
  1              5              10              15

atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc ctg gtg gac ggc 96
Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu Val Asp Gly
              20              25              30

cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag ggc ctc acc acc 144
His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly Leu Thr Thr
              35              40              45

agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc gcc aag agc ctc 192
Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala Lys Ser Leu
              50              55              60

ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc gtg gtc ttt gac 240
Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val Val Phe Asp
              65              70              75              80

gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg ggg tac aag gcg 288
Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly Tyr Lys Ala
              85              90              95

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ggc cgg gcc ccc acg ctc gtc ccg cgc ggc tcc gag gac ttt ccc cgg	336
Gly Arg Ala Pro Thr Leu Val Pro Arg Gly Ser Glu Asp Phe Pro Arg	
100 105 110	
caa ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc	384
Gln Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg	
115 120 125	
ctc gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc	432
Leu Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala	
130 135 140	
aag aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac	480
Lys Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp	
145 150 155 160	
aaa gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc	528
Lys Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro	
165 170 175	
gag ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg	576
Glu Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu	
180 185 190	
agg ccc gac cag tgg gcc gac tac ccg gcc ctg acc ggg gac gag tcc	624
Arg Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser	
195 200 205	
gac aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag	672
Asp Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys	
210 215 220	
ctt ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac	720
Leu Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp	
225 230 235 240	
cgg ctg aag ccc gcc atc ccg gag aag atc ctg gcc cac atg gac gat	768
Arg Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp	
245 250 255	
ctg aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg	816
Leu Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu	
260 265 270	
gag gtg gac ttc gcc aaa agg ccg gag ccc gac cgg gag agg ctt agg	864
Glu Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg	
275 280 285	
gcc ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc	912
Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly	
290 295 300	
ctt ctg gaa agc ccc aag gcc gca ctc gag cac cac cac cac cac	960
Leu Leu Glu Ser Pro Lys Ala Ala Leu Glu His His His His His	
305 310 315 320	
tga	963

<210> 102
 <211> 320
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 102

Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Gln	Met	Gly	Arg	Ile	Asn	Ser	Gly	1	5	10	15
Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu	Val	Asp	Gly	20	25	30	
His	His	Leu	Ala	Tyr	Arg	Thr	Phe	His	Ala	Leu	Lys	Gly	Leu	Thr	Thr	35	40	45	
Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala	Lys	Ser	Leu	50	55	60	
Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Asp	Ala	Val	Ile	Val	Val	Phe	Asp	65	70	75	80
Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Gly	Gly	Tyr	Lys	Ala	85	90	95	
Gly	Arg	Ala	Pro	Thr	Leu	Val	Pro	Arg	Gly	Ser	Glu	Asp	Phe	Pro	Arg	100	105	110	
Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Leu	Ala	Arg	115	120	125	
Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Ser	Leu	Ala	130	135	140	
Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	145	150	155	160
Lys	Asp	Leu	Tyr	Gln	Leu	Leu	Ser	Asp	Arg	Ile	His	Val	Leu	His	Pro	165	170	175	
Glu	Gly	Tyr	Leu	Ile	Thr	Pro	Ala	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	180	185	190	
Arg	Pro	Asp	Gln	Trp	Ala	Asp	Tyr	Arg	Ala	Leu	Thr	Gly	Asp	Glu	Ser	195	200	205	
Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Arg	Lys	210	215	220	
Leu	Leu	Glu	Glu	Trp	Gly	Ser	Leu	Glu	Ala	Leu	Leu	Lys	Asn	Leu	Asp	225	230	235	240
Arg	Leu	Lys	Pro	Ala	Ile	Arg	Glu	Lys	Ile	Leu	Ala	His	Met	Asp	Asp	245	250	255	
Leu	Lys	Leu	Ser	Trp	Asp	Leu	Ala	Lys	Val	Arg	Thr	Asp	Leu	Pro	Leu	260	265	270	
Glu	Val	Asp	Phe	Ala	Lys	Arg	Arg	Glu	Pro	Asp	Arg	Glu	Arg	Leu	Arg	275	280	285	

Ala Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly
290 295 300

Leu Leu Glu Ser Pro Lys Ala Ala Leu Glu His His His His His His
305 310 315 320

<210> 103
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 103
cgatctcctc ggccacctcc 20

<210> 104
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 104
ggcggtgccc tggacgggca 20

<210> 105
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 105
ccagctcggt gtggacctga 20

<210> 106
<211> 2505
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1) .. (2499)

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 106
atg aat tcg ggg atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc 48
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag	96
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys	
20 25 30	
ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc	144
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe	
35 40 45	
gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc	192
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile	
50 55 60	
gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg	240
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly	
65 70 75 80	
ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa	288
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln	
85 90 95	
ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc	336
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu	
100 105 110	
gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag	384
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys	
115 120 125	
aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa	432
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys	
130 135 140	
gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag	480
Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu	
145 150 155 160	
ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg	528
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg	
165 170 175	
ccc gac cag tgg gcc gac tac ccg gcc ctg acc ggg gac gag tcc gac	576
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp	
180 185 190	
aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag ctt	624
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu	
195 200 205	
ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac cgg	672
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg	
210 215 220	
ctg aag ccc gcc atc ccg gag aag atc ctg gcc cac atg gac gat ctg	720
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu	
225 230 235 240	
aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg gag	768
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu	
245 250 255	

gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg gcc	816
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala	
260 265 270	
ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt	864
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu	
275 280 285	
ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa	912
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu	
290 295 300	
ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc	960
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala	
305 310 315 320	
gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc	1008
Asp Leu Leu Ala Leu Ala Ala Arg Gly Gly Arg Val His Arg Ala	
325 330 335	
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt	1056
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu	
340 345 350	
ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc	1104
Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu	
355 360 365	
ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc	1152
Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser	
370 375 380	
aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg	1200
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr	
385 390 395 400	
gag gag gcg ggg gag cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac	1248
Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn	
405 410 415	
ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cgg	1296
Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg	
420 425 430	
gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg	1344
Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr	
435 440 445	
ggg gtg cgc ctg gac gtg gcc tat ctc agg gcc ttg tcc ctg gag gtg	1392
Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val	
450 455 460	
gcc gag gag atc gcc cgc ctc gag gcc gag gtc ttc cgc ctg gcc ggc	1440
Ala Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly	
465 470 475 480	
cac ccc ttc aac ctc aac tcc cgg gac cag ctg gaa agg gtc ctc ttt	1488
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe	
485 490 495	

gac Asp	gag Glu	cta Leu	ggg Gly 500	ctt Leu	ccc Pro	gcc Ala	atc Ile	ggc Gly 505	aag Lys	acg Thr	gag Glu	aag Lys	acc Thr 510	ggc Gly	aag Lys	1536
cgc Arg	tcc Ser	acc Thr 515	agc Ser	gcc Ala	gcc Ala	gtc Val 520	ctg Leu	gag Glu	gcc Ala	ctc Leu	cgc Arg	gag Glu 525	gcc Ala	cac His	ccc Pro	1584
atc Ile	gtg Val 530	gag Glu	aag Lys	atc Ile	ctg Leu	cag Gln 535	tac Tyr	cgg Arg	gag Glu	ctc Leu	acc Thr 540	aag Lys	ctg Leu	aag Lys	agc Ser	1632
acc Thr 545	tac Tyr	att Ile	gac Asp	ccc Pro	ttg Leu 550	cgc Pro	gac Asp	ctc Leu	atc Ile	cac His 555	ccc Pro	agg Arg	acg Thr	ggc Gly	cgc Arg 560	1680
ctc Leu	cac His	acc Thr	cgc Arg	ttc Phe 565	aac Asn	cag Gln	acg Thr	gcc Ala 570	acg Thr	gcc Ala	acg Thr	ggc Gly	agg Arg	cta Leu 575	agt Ser	1728
agc Ser	tcc Ser	gat Asp	ccc Pro 580	aac Asn	ctc Leu	cag Gln	aac Asn	atc Ile 585	ccc Pro	gtc Val	cgc Arg	acc Thr 590	ccg Pro	ctt Leu	ggg Gly	1776
cag Gln	agg Arg	atc Ile 595	cgc Arg	cgg Arg	gcc Ala	ttc Phe	atc Ile 600	gcc Ala	gag Glu	gag Glu	ggg Gly	tgg Trp 605	cta Leu	ttg Leu	gtg Val	1824
gcc Ala 610	ctg Leu	gac Asp	tat Tyr	agc Ser	cag Gln	ata Ile 615	gag Glu	ctc Leu	agg Arg	gtg Val	ctg Leu 620	gcc Ala	cac His	ctc Leu	tcc Ser	1872
ggc Gly 625	gac Asp	gag Glu	aac Asn	ctg Leu	atc Ile 630	cgg Arg	gtc Val	ttc Phe	cag Gln	gag Glu 635	ggg Gly	cgg Arg	gac Asp	atc Ile	cac His 640	1920
acg Thr	gag Glu	acc Thr	gcc Ala	agc Ser 645	tgg Trp	atg Met	ttc Phe	ggc Gly	gtc Val 650	ccc Pro	cgg Arg	gag Glu	gcc Ala	gtg Val 655	gac Asp	1968
ccc Pro	ctg Leu	atg Met	cgc Arg 660	cgg Arg	gcg Ala	gcc Ala	aag Lys	acc Thr 665	atc Ile	aac Asn	ttc Phe	ggg Gly 670	gtc Val	ctc Leu	tac Tyr	2016
ggc Gly	atg Met	tgc Ser 675	gcc Ala	cac His	cgc Arg	ctc Leu	tcc Ser 680	cag Gln	gag Glu	cta Leu	gcc Ala 685	atc Ile	cct Pro	tac Tyr	gag Glu	2064
gag Glu 690	gcc Ala	cag Gln	gcc Ala	ttc Phe	att Ile	gag Glu 695	cgc Arg	tac Tyr	ttt Phe	cag Gln 700	agc Ser	ttc Phe	ccc Pro	aag Lys	gtg Val	2112
cgg Arg 705	gcc Ala	tgg Trp	att Ile	gag Glu	aag Lys 710	acc Thr	ctg Leu	gag Glu	gag Glu	ggc Gly 715	agg Arg	agg Arg	cgg Arg	ggg Gly	tac Tyr 720	2160
gtg Val	gag Glu	acc Thr	ctc Leu	ttc Phe 725	ggc Gly	cgc Arg	cgc Arg	cgc Arg	tac Tyr 730	gtg Val	cca Pro	gac Asp	cta Leu	gag Glu 735	gcc Ala	2208

cgg gtg aag agc gtg cgg gag gcg gcc gag cgc atg gcc ttc aac atg	2256
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met	
740 745 750	
ccc gtc cag ggc acc gcc gcc gac ctc atg aag ctg gct atg gtg aag	2304
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys	
755 760 765	
ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc	2352
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val	
770 775 780	
cac aac gag ctg gtc ctc gag gcc cca aaa gag agg gcg gag gcc gtg	2400
His Asn Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val	
785 790 795 800	
gcc cgg ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg	2448
Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val	
805 810 815	
ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag	2496
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys	
820 825 830	
gag tgatag	2505
Glu	

<210> 107
 <211> 833
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 107
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125

Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270
 Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
 275 280 285
 Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
 290 295 300
 Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
 305 310 315 320
 Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
 325 330 335
 Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
 340 345 350
 Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
 355 360 365
 Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
 370 375 380
 Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
 385 390 395 400
 Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460

Ala	Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	465	470	475	480
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	485	490	495	
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	500	505	510	
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	515	520	525	
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	530	535	540	
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	545	550	555	560
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	565	570	575	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	580	585	590	
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val	595	600	605	
Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser	610	615	620	
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His	625	630	635	640
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp	645	650	655	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr	660	665	670	
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu	675	680	685	
Glu	Ala	Gln	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	Pro	Lys	Val	690	695	700	
Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Arg	Arg	Gly	Tyr	705	710	715	720
Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	Leu	Glu	Ala	725	730	735	
Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	Phe	Asn	Met	740	745	750	
Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	Met	Val	Lys	755	760	765	
Leu	Phe	Pro	Arg	Leu	Glu	Glu	Met	Gly	Ala	Arg	Met	Leu	Leu	Gln	Val	770	775	780	
His	Asn	Glu	Leu	Val	Leu	Glu	Ala	Pro	Lys	Glu	Arg	Ala	Glu	Ala	Val	785	790	795	800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu

<210> 108

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 108

gggataccat gggagtgcag tttgg

25

<210> 109

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 109

ggtaaatttt tctcgtcgac atccac

27

<210> 110

<211> 981

<212> DNA

<213> Methanococcus jannaschii

<220>

<221> CDS

<222> (1) .. (978)

<400> 110

atg gga gtg cag ttt ggt gat ttt att cca aaa aat att atc tcc ttt 48
Met Gly Val Gln Phe Gly Asp Phe Ile Pro Lys Asn Ile Ile Ser Phe
1 5 10 15

gaa gat tta aaa ggg aaa aaa gta gct att gat gga atg aat gca tta 96
Glu Asp Leu Lys Gly Lys Lys Val Ala Ile Asp Gly Met Asn Ala Leu
20 25 30

tat cag ttt tta aca tct ata cgt ttg aga gat ggt tct cca ttg aga 144
Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg
35 40 45

aat aga aaa gga gag ata acc tca gca tat aac gga gtt ttt tat aaa 192
Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys
50 55 60

acc	ata	cat	ttg	tta	gag	aat	gat	ata	act	cca	atc	tgg	gtt	ttt	gat	240
Thr	Ile	His	Leu	Leu	Glu	Asn	Asp	Ile	Thr	Pro	Ile	Trp	Val	Phe	Asp	
65					70					75					80	
ggt	gag	cca	cca	aag	tta	aag	gag	aaa	aca	agg	aaa	gtt	agg	aga	gag	288
Gly	Glu	Pro	Pro	Lys	Leu	Lys	Glu	Lys	Thr	Arg	Lys	Val	Arg	Arg	Glu	
				85					90					95		
atg	aaa	gag	aaa	gct	gaa	ctt	aag	atg	aaa	gag	gca	att	aaa	aag	gag	336
Met	Lys	Glu	Lys	Ala	Glu	Leu	Lys	Met	Lys	Glu	Ala	Ile	Lys	Lys	Glu	
			100					105					110			
gat	ttt	gaa	gaa	gct	gct	aag	tat	gca	aag	agg	gtt	agc	tat	cta	act	384
Asp	Phe	Glu	Glu	Ala	Ala	Lys	Tyr	Ala	Lys	Arg	Val	Ser	Tyr	Leu	Thr	
		115					120					125				
ccg	aaa	atg	gtt	gaa	aac	tgc	aaa	tat	ttg	tta	agt	ttg	atg	ggc	att	432
Pro	Lys	Met	Val	Glu	Asn	Cys	Lys	Tyr	Leu	Leu	Ser	Leu	Met	Gly	Ile	
	130					135					140					
ccg	tat	gtt	gaa	gct	ccc	tct	gag	gga	gag	gca	caa	gca	agc	tat	atg	480
Pro	Tyr	Val	Glu	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ser	Tyr	Met	
145					150					155					160	
gca	aag	aag	gga	gat	gtt	tgg	gca	gtt	gta	agt	caa	gat	tat	gat	gcc	528
Ala	Lys	Lys	Gly	Asp	Val	Trp	Ala	Val	Val	Ser	Gln	Asp	Tyr	Asp	Ala	
				165					170					175		
ttg	tta	tat	gga	gct	ccg	aga	gtt	gtt	aga	aat	tta	aca	act	aca	aag	576
Leu	Leu	Tyr	Gly	Ala	Pro	Arg	Val	Val	Arg	Asn	Leu	Thr	Thr	Thr	Lys	
			180					185					190			
gag	atg	cca	gaa	ctt	att	gaa	tta	aat	gag	gtt	tta	gag	gat	tta	aga	624
Glu	Met	Pro	Glu	Leu	Ile	Glu	Leu	Asn	Glu	Val	Leu	Glu	Asp	Leu	Arg	
		195					200					205				
att	tct	ttg	gat	gat	ttg	ata	gat	ata	gcc	ata	ttt	atg	gga	act	gac	672
Ile	Ser	Leu	Asp	Asp	Leu	Ile	Asp	Ile	Ala	Ile	Phe	Met	Gly	Thr	Asp	
	210					215					220					
tat	aat	cca	gga	gga	gtt	aaa	gga	ata	gga	ttt	aaa	agg	gct	tat	gaa	720
Tyr	Asn	Pro	Gly	Gly	Val	Lys	Gly	Ile	Gly	Phe	Lys	Arg	Ala	Tyr	Glu	
225					230					235					240	
ttg	gtt	aga	agt	ggt	gta	gct	aag	gat	gtt	ttg	aaa	aaa	gag	gtt	gaa	768
Leu	Val	Arg	Ser	Gly	Val	Ala	Lys	Asp	Val	Leu	Lys	Lys	Glu	Val	Glu	
				245					250					255		
tac	tac	gat	gag	att	aag	agg	ata	ttt	aaa	gag	cca	aag	gtt	acc	gat	816
Tyr	Tyr	Asp	Glu	Ile	Lys	Arg	Ile	Phe	Lys	Glu	Pro	Lys	Val	Thr	Asp	
			260					265					270			
aac	tat	tca	tta	agc	cta	aaa	ttg	cca	gat	aaa	gag	gga	att	ata	aaa	864
Asn	Tyr	Ser	Leu	Ser	Leu	Lys	Leu	Pro	Asp	Lys	Glu	Gly	Ile	Ile	Lys	
		275					280					285				
ttc	tta	gtt	gat	gaa	aat	gac	ttt	aat	tat	gat	agg	gtt	aaa	aag	cat	912
Phe	Leu	Val	Asp	Glu	Asn	Asp	Phe	Asn	Tyr	Asp	Arg	Val	Lys	Lys	His	
	290					295					300					

gtt gat aaa ctc tat aac tta att gca aac aaa act aag caa aaa aca 960
 Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr
 305 310 315 320

tta gat gca tgg ttt aaa taa 981
 Leu Asp Ala Trp Phe Lys
 325

<210> 111
 <211> 326
 <212> PRT
 <213> Methanococcus jannaschii

<400> 111
 Met Gly Val Gln Phe Gly Asp Phe Ile Pro Lys Asn Ile Ile Ser Phe
 1 5 10 15
 Glu Asp Leu Lys Gly Lys Lys Val Ala Ile Asp Gly Met Asn Ala Leu
 20 25 30
 Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg
 35 40 45
 Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys
 50 55 60
 Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp
 65 70 75 80
 Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu
 85 90 95
 Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu
 100 105 110
 Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr
 115 120 125
 Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile
 130 135 140
 Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met
 145 150 155 160
 Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala
 165 170 175
 Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Thr Lys
 180 185 190
 Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg
 195 200 205
 Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp
 210 215 220
 Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu
 225 230 235 240
 Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu
 245 250 255

Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp
 260 265 270
 Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys
 275 280 285
 Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His
 290 295 300
 Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr
 305 310 315 320
 Leu Asp Ala Trp Phe Lys
 325

<210> 112
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 112
 gaggtgatac catgggtgta c 21

<210> 113
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 113
 gaaactctgc agcgcgtcag 20

<210> 114
 <211> 1023
 <212> DNA
 <213> Pyrococcus furiosus

<220>
 <221> CDS
 <222> (1)..(1020)

<400> 114
 atg ggt gtc cca att ggt gag att ata cca aga aaa gaa att gag tta 48
 Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu
 1 5 10 15
 gaa aac cta tac ggg aaa aaa atc gca atc gac gct ctt aat gca atc 96
 Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile
 20 25 30
 tac caa ttt ttg tcc aca ata aga cag aaa gat gga act cca ctt atg 144
 Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met
 35 40 45

gat tca aag ggt aga ata acc tcc cac cta agc ggg ctc ttt tac agg	192
Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg	
50 55 60	
aca ata aac cta atg gag gct gga ata aaa cct gtg tat gtt ttt gat	240
Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp	
65 70 75 80	
gga gaa cct cca gaa ttc aaa aag aaa gag ctc gaa aaa aga aga gaa	288
Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu	
85 90 95	
gcg aga gag gaa gct gaa gaa aag tgg aga gaa gca ctt gaa aaa gga	336
Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly	
100 105 110	
gag ata gag gaa gca aga aaa tat gcc caa aga gca acc agg gta aat	384
Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn	
115 120 125	
gaa atg ctc atc gag gat gca aaa aaa ctc tta gag ctt atg gga att	432
Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile	
130 135 140	
cct ata gtt caa gca cct agc gag gga gag gcc caa gct gca tat atg	480
Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met	
145 150 155 160	
gcc gca aag ggg agc gtg tat gca tcg gct agt caa gat tac gat tcc	528
Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser	
165 170 175	
cta ctt ttt gga gct cca aga ctt gtt aga aac tta aca ata aca gga	576
Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly	
180 185 190	
aaa aga aag ttg cct ggg aaa aat gtc tac gtc gag ata aag ccc gag	624
Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu	
195 200 205	
ttg ata att ttg gag gaa gta ctc aag gaa tta aag cta aca aga gaa	672
Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu	
210 215 220	
aag ctc att gaa cta gca atc ctc gtt gga aca gac tac aac cca gga	720
Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly	
225 230 235 240	
gga ata aag ggc ata ggc ctt aaa aaa gct tta gag att gtt aga cac	768
Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His	
245 250 255	
tca aaa gat ccg cta gca aag ttc caa aag caa agc gat gtg gat tta	816
Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu	
260 265 270	
tat gca ata aaa gag ttc ttc cta aac cca cca gtc aca gat aac tac	864
Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr	
275 280 285	

aat tta gtg tgg aga gat ccc gac gaa gag gga ata cta aag ttc tta	912
Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu	
290 295 300	
tgt gac gag cat gac ttt agt gag gaa aga gta aag aat gga tta gag	960
Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu	
305 310 315 320	
agg ctt aag aag gca atc aaa agt gga aaa caa tca acc ctt gaa agt	1008
Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser	
325 330 335	
tgg ttc aag aga taa	1023
Trp Phe Lys Arg	
340	

<210> 115
 <211> 340
 <212> PRT
 <213> *Pyrococcus furiosus*

<400> 115	
Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu	
1 5 10 15	
Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile	
20 25 30	
Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met	
35 40 45	
Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg	
50 55 60	
Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp	
65 70 75 80	
Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu	
85 90 95	
Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly	
100 105 110	
Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn	
115 120 125	
Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile	
130 135 140	
Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met	
145 150 155 160	
Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser	
165 170 175	
Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly	
180 185 190	
Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu	
195 200 205	

Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu
 210 215 220
 Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly
 225 230 235 240
 Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His
 245 250 255
 Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu
 260 265 270
 Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr
 275 280 285
 Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu
 290 295 300
 Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu
 305 310 315 320
 Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser
 325 330 335
 Trp Phe Lys Arg
 340

<210> 116
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 116
 gataccatgg gtgtcccaat tgggtg

25

<210> 117
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 117
 tcgacgtcga cttatctctt gaaccaactt tcaaggg

37

<210> 118
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 118
 agcgaggagg aggcccaagc

20

<210> 119
 <211> 21
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 119
 gcctatgccc tttattcctc c 21

<210> 120
 <211> 33
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 120
 tggtcgctgt ctcgctgaaa gcgagacagc gtg 33

<210> 121
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 121
 tgctctctgg tcgctgtctg aaagacagcg 30

<210> 122
 <211> 14
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 122
 cgagagacca cgct 14

<210> 123
 <211> 44
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 123
 ttttccagag cctaataaaa ttaggctctg gaaagacgct cgtg 44

<210> 124
 <211> 14
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 124
 aacgagcgtc tttg 14

<210> 125
 <211> 14
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 125
 aacgagcgtc attg 14

<210> 126
 <211> 51
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 126
 ttttttttta attaggctct ggaaagacgc tcgtgaaacg agcgtctttg d 51

<210> 127
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 127
 ttttccagag cctaag 17

<210> 128
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 128
 tggctatagr ccagggccac 20

<210> 129
 <211> 2505
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(2499)

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 129
 atg aat tcg ggg atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc 48
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag 96
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc 144
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc 192
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg 240
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa 288
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc 336
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag 384
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa 432
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag 480
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg 528
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 ccc gac cag tgg gcc gac tac ccg gcc ctg acc ggg gac gag tcc gac 576
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190

aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag ctt	624
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu	
195 200 205	
ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac cgg	672
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg	
210 215 220	
ctg aag ccc gcc atc cgg gag aag atc ctg gcc cac atg gac gat ctg	720
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu	
225 230 235 240	
aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg gag	768
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu	
245 250 255	
gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg gcc	816
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala	
260 265 270	
ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt	864
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu	
275 280 285	
ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa	912
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu	
290 295 300	
ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc	960
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala	
305 310 315 320	
gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc	1008
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala	
325 330 335	
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt	1056
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu	
340 345 350	
ctc gcc aaa gac ctg agc gtt ctg gcc ctg agg gaa ggc ctt ggc ctc	1104
Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu	
355 360 365	
ccg ccc ggc gac gac ccc atg ctc ctc gcc tac ctc ctg gac cct tcc	1152
Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser	
370 375 380	
aac acc acc ccc gag ggg gtg gcc cgg cgc tac ggc ggg gag tgg acg	1200
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr	
385 390 395 400	
gag gag gcg ggg gag cgg gcc gcc ctt tcc gag agg ctc ttc gcc aac	1248
Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn	
405 410 415	
ctg tgg ggg agg ctt gag ggg gag gag agg ctc ctt tgg ctt tac cgg	1296
Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg	
420 425 430	
gag gtg gag agg ccc ctt tcc gct gtc ctg gcc cac atg gag gcc acg	1344
Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr	

435					440					445							
ggg	gtg	cgc	ctg	gac	gtg	gcc	tat	ctc	agg	gcc	ttg	tcc	ctg	gag	gtg	1392	
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val		
450					455					460							
gcc	ggg	gag	atc	gcc	cgc	ctc	gag	gcc	gag	gtc	ttc	cgc	ctg	gcc	ggc	1440	
Ala	Gly	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly		
465					470					475					480		
cac	ccc	ttc	aac	ctc	aac	tcc	cgg	gac	cag	ctg	gaa	agg	gtc	ctc	ttt	1488	
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe		
485					490					495							
gac	gag	cta	ggg	ctt	ccc	gcc	atc	ggc	aag	acg	gag	aag	acc	ggc	aag	1536	
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys		
500					505					510							
cgc	tcc	acc	agc	gcc	gcc	gtc	ctg	gag	gcc	ctc	cgc	gag	gcc	cac	ccc	1584	
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro		
515					520					525							
atc	gtg	gag	aag	atc	ctg	cag	tac	cgg	gag	ctc	acc	aag	ctg	aag	agc	1632	
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser		
530					535					540							
acc	tac	att	gac	ccc	ttg	ccg	gac	ctc	atc	cac	ccc	agg	acg	ggc	cgc	1680	
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg		
545					550					555					560		
ctc	cac	acc	cgc	ttc	aac	cag	acg	gcc	acg	gcc	acg	ggc	agg	cta	agt	1728	
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser		
565					570					575							
agc	tcc	gat	ccc	aac	ctc	cag	aac	atc	ccc	gtc	cgc	acc	ccg	ctt	ggg	1776	
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly		
580					585					590							
cag	agg	atc	cgc	cgg	gcc	ttc	atc	gcc	gag	gag	ggg	tgg	cta	ttg	gtg	1824	
Gln	Arg	Ile	Arg	Arg	Ala	Phe	Ile	Ala	Glu	Glu	Gly	Trp	Leu	Leu	Val		
595					600					605							
gcc	ctg	gcc	tat	agc	cag	ata	gag	ctc	agg	gtg	ctg	gcc	cac	ctc	tcc	1872	
Ala	Leu	Ala	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	His	Leu	Ser		
610					615					620							
ggc	gac	gag	aac	ctg	atc	cgg	gtc	ttc	cag	gag	ggg	cgg	gac	atc	cac	1920	
Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Arg	Asp	Ile	His		
625					630					635					640		
acg	gag	acc	gcc	agc	tgg	atg	ttc	ggc	gtc	ccc	cgg	gag	gcc	gtg	gac	1968	
Thr	Glu	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Arg	Glu	Ala	Val	Asp		
645					650					655							
ccc	ctg	atg	cgc	cgg	gcg	gcc	aag	acc	atc	aac	ttc	ggg	gtc	ctc	tac	2016	
Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Ile	Asn	Phe	Gly	Val	Leu	Tyr		
660					665					670							
ggc	atg	tcg	gcc	cac	cgc	ctc	tcc	cag	gag	cta	gcc	atc	cct	tac	gag	2064	
Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	Pro	Tyr	Glu		
675					680					685							

gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg	2112
Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val	
690 695 700	
cgg gcc tgg att gag aag acc ctg gag gag ggc agg agg cgg ggg tac	2160
Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr	
705 710 715 720	
gtg gag acc ctc ttc ggc cgc cgc cgc tac gtg cca gac cta gag gcc	2208
Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala	
725 730 735	
cgg gtg aag agc gtg cgg gag gcg gcc gag cgc atg gcc ttc aac atg	2256
Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met	
740 745 750	
ccc gtc cag ggc acc gcc gcc gac ctc atg aag ctg gct atg gtg aag	2304
Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys	
755 760 765	
ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc	2352
Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val	
770 775 780	
cac gac gag ctg gtc ctc gag gcc cca aaa gag agg gcg gag gcc gtg	2400
His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val	
785 790 795 800	
gcc cgg ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg	2448
Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val	
805 810 815	
ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag	2496
Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys	
820 825 830	
gag tgatag	2505
Glu	

<210> 130

<211> 833

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 130

Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

Val 65	Val	Phe	Asp	Ala	Lys 70	Ala	Pro	Ser	Phe	Arg 75	His	Glu	Ala	Tyr	Gly 80
Gly	Tyr	Lys	Ala	Gly 85	Arg	Ala	Pro	Thr	Pro 90	Glu	Asp	Phe	Pro	Arg 95	Gln
Leu	Ala	Leu	Ile 100	Lys	Glu	Leu	Val	Asp 105	Leu	Leu	Gly	Leu	Ala	Arg	Leu
Glu	Val	Pro 115	Gly	Tyr	Glu	Ala	Asp 120	Asp	Val	Leu	Ala	Ser 125	Leu	Ala	Lys
Lys 130	Ala	Glu	Lys	Glu	Gly	Tyr 135	Glu	Val	Arg	Ile	Leu 140	Thr	Ala	Asp	Lys
Asp 145	Leu	Tyr	Gln	Leu	Leu	Ser 150	Asp	Arg	Ile	His 155	Val	Leu	His	Pro	Glu 160
Gly	Tyr	Leu	Ile 165	Thr	Pro	Ala	Trp	Leu	Trp 170	Glu	Lys	Tyr	Gly	Leu	Arg
Pro	Asp	Gln	Trp 180	Ala	Asp	Tyr	Arg	Ala 185	Leu	Thr	Gly	Asp	Glu	Ser	Asp
Asn	Leu	Pro 195	Gly	Val	Lys	Gly	Ile 200	Gly	Glu	Lys	Thr	Ala 205	Arg	Lys	Leu
Leu	Glu 210	Glu	Trp	Gly	Ser	Leu 215	Glu	Ala	Leu	Leu	Lys 220	Asn	Leu	Asp	Arg
Leu 225	Lys	Pro	Ala	Ile	Arg 230	Glu	Lys	Ile	Leu	Ala 235	His	Met	Asp	Asp	Leu 240
Lys	Leu	Ser	Trp	Asp 245	Leu	Ala	Lys	Val	Arg 250	Thr	Asp	Leu	Pro	Leu	Glu 255
Val	Asp	Phe	Ala 260	Lys	Arg	Arg	Glu	Pro 265	Asp	Arg	Glu	Arg	Leu	Arg	Ala
Phe	Leu	Glu 275	Arg	Leu	Glu	Phe	Gly 280	Ser	Leu	Leu	His	Glu 285	Phe	Gly	Leu
Leu	Glu 290	Ser	Pro	Lys	Ala	Leu 295	Glu	Glu	Ala	Pro	Trp 300	Pro	Pro	Pro	Glu
Gly 305	Ala	Phe	Val	Gly	Phe 310	Val	Leu	Ser	Arg	Lys 315	Glu	Pro	Met	Trp	Ala 320
Asp	Leu	Leu	Ala	Leu 325	Ala	Ala	Ala	Arg	Gly 330	Gly	Arg	Val	His	Arg 335	Ala
Pro	Glu	Pro	Tyr 340	Lys	Ala	Leu	Arg	Asp 345	Leu	Lys	Glu	Ala	Arg	Gly	Leu
Leu	Ala	Lys 355	Asp	Leu	Ser	Val	Leu 360	Ala	Leu	Arg	Glu	Gly 365	Leu	Gly	Leu
Pro	Pro 370	Gly	Asp	Asp	Pro	Met 375	Leu	Leu	Ala	Tyr	Leu 380	Leu	Asp	Pro	Ser
Asn 385	Thr	Thr	Pro	Glu	Gly 390	Val	Ala	Arg	Arg	Tyr 395	Gly	Gly	Glu	Trp	Thr 400

Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
 405 410 415
 Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
 420 425 430
 Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
 435 440 445
 Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
 450 455 460
 Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
 465 470 475 480
 His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
 485 490 495
 Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
 500 505 510
 Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
 515 520 525
 Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
 530 535 540
 Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
 545 550 555 560
 Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
 565 570 575
 Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
 580 585 590
 Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
 595 600 605
 Ala Leu Ala Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735

Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
740 745 750

Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
755 760 765

Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
770 775 780

His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
785 790 795 800

Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
805 810 815

Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
820 825 830

Glu

<210> 131
<211> 2505
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1) .. (2499)

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 131
atg aat tcg ggg atg ctg ccc ctc ttt gag ccc aag ggc cgg gtc ctc 48
Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
1 5 10 15

ctg gtg gac ggc cac cac ctg gcc tac cgc acc ttc cac gcc ctg aag 96
Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
20 25 30

ggc ctc acc acc agc cgg ggg gag ccg gtg cag gcg gtc tac ggc ttc 144
Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
35 40 45

gcc aag agc ctc ctc aag gcc ctc aag gag gac ggg gac gcg gtg atc 192
Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
50 55 60

gtg gtc ttt gac gcc aag gcc ccc tcc ttc cgc cac gag gcc tac ggg 240
Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
65 70 75 80

ggg tac aag gcg ggc cgg gcc ccc acg ccg gag gac ttt ccc cgg caa 288
Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
85 90 95

ctc gcc ctc atc aag gag ctg gtg gac ctc ctg ggg ctg gcg cgc ctc 336
Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
100 105 110

gag gtc ccg ggc tac gag gcg gac gac gtc ctg gcc agc ctg gcc aag	384
Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys	
115 120 125	
aag gcg gaa aag gag ggc tac gag gtc cgc atc ctc acc gcc gac aaa	432
Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys	
130 135 140	
gac ctt tac cag ctc ctt tcc gac cgc atc cac gtc ctc cac ccc gag	480
Asp Leu Tyr Gln Leu Ser Asp Arg Ile His Val Leu His Pro Glu	
145 150 155 160	
ggg tac ctc atc acc ccg gcc tgg ctt tgg gaa aag tac ggc ctg agg	528
Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg	
165 170 175	
ccc gac cag tgg gcc gac tac cgg gcc ctg acc ggg gac gag tcc gac	576
Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp	
180 185 190	
aac ctt ccc ggg gtc aag ggc atc ggg gag aag acg gcg agg aag ctt	624
Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu	
195 200 205	
ctg gag gag tgg ggg agc ctg gaa gcc ctc ctc aag aac ctg gac cgg	672
Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg	
210 215 220	
ctg aag ccc gcc atc cgg gag aag atc ctg gcc cac atg gac gat ctg	720
Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu	
225 230 235 240	
aag ctc tcc tgg gac ctg gcc aag gtg cgc acc gac ctg ccc ctg gag	768
Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu	
245 250 255	
gtg gac ttc gcc aaa agg cgg gag ccc gac cgg gag agg ctt agg gcc	816
Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala	
260 265 270	
ttt ctg gag agg ctt gag ttt ggc agc ctc ctc cac gag ttc ggc ctt	864
Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu	
275 280 285	
ctg gaa agc ccc aag gcc ctg gag gag gcc ccc tgg ccc ccg ccg gaa	912
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu	
290 295 300	
ggg gcc ttc gtg ggc ttt gtg ctt tcc cgc aag gag ccc atg tgg gcc	960
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala	
305 310 315 320	
gat ctt ctg gcc ctg gcc gcc gcc agg ggg ggc cgg gtc cac cgg gcc	1008
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala	
325 330 335	
ccc gag cct tat aaa gcc ctc agg gac ctg aag gag gcg cgg ggg ctt	1056
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu	
340 345 350	

ctc	gcc	aaa	gac	ctg	agc	gtt	ctg	gcc	ctg	agg	gaa	ggc	ctt	ggc	ctc	1104
Leu	Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	
		355					360					365				
ccg	ccc	ggc	gac	gac	ccc	atg	ctc	ctc	gcc	tac	ctc	ctg	gac	cct	tcc	1152
Pro	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	
		370				375					380					
aac	acc	acc	ccc	gag	ggg	gtg	gcc	cgg	cgc	tac	ggc	ggg	gag	tgg	acg	1200
Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	
		385			390					395					400	
gag	gag	gcg	ggg	gag	cgg	gcc	gcc	ctt	tcc	gag	agg	ctc	ttc	gcc	aac	1248
Glu	Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	
				405					410					415		
ctg	tgg	ggg	agg	ctt	gag	ggg	gag	gag	agg	ctc	ctt	tgg	ctt	tac	cgg	1296
Leu	Trp	Gly	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	
			420					425					430			
gag	gtg	gag	agg	ccc	ctt	tcc	gct	gtc	ctg	gcc	cac	atg	gag	gcc	acg	1344
Glu	Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	
		435					440					445				
ggg	gtg	cgc	ctg	gac	gtg	gcc	tat	ctc	agg	gcc	ttg	tcc	ctg	gag	gtg	1392
Gly	Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	
	450					455					460					
gcc	ggg	gag	atc	gcc	cgc	ctc	gag	gcc	gag	gtc	ttc	cgc	ctg	gcc	ggc	1440
Ala	Gly	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	
	465				470					475					480	
cac	ccc	ttc	aac	ctc	aac	tcc	cgg	gac	cag	ctg	gaa	agg	gtc	ctc	ttt	1488
His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	
				485				490						495		
gac	gag	cta	ggg	ctt	ccc	gcc	atc	ggc	aag	acg	gag	aag	acc	ggc	aag	1536
Asp	Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	
			500					505					510			
cgc	tcc	acc	agc	gcc	gcc	gtc	ctg	gag	gcc	ctc	cgc	gag	gcc	cac	ccc	1584
Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	
		515				520						525				
atc	gtg	gag	aag	atc	ctg	cag	tac	cgg	gag	ctc	acc	aag	ctg	aag	agc	1632
Ile	Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	
	530					535					540					
acc	tac	att	gac	ccc	ttg	ccg	gac	ctc	atc	cac	ccc	agg	acg	ggc	cgc	1680
Thr	Tyr	Ile	Asp	Pro	Leu	Pro	Asp	Leu	Ile	His	Pro	Arg	Thr	Gly	Arg	
	545				550					555					560	
ctc	cac	acc	cgc	ttc	aac	cag	acg	gcc	acg	gcc	acg	ggc	agg	cta	agt	1728
Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	Arg	Leu	Ser	
				565				570						575		
agc	tcc	gat	ccc	aac	ctc	cag	aac	atc	ccc	gtc	cgc	acc	ccg	ctt	ggg	1776
Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	Pro	Leu	Gly	
			580					585					590			

cag agg atc cgc cgg gcc ttc atc gcc gag gag ggg tgg cta ttg gtg Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val 595 600 605	1824
gcc ctg gtc tat agc cag ata gag ctc agg gtg ctg gcc cac ctc tcc Ala Leu Val Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser 610 615 620	1872
ggc gac gag aac ctg atc cgg gtc ttc cag gag ggg cgg gac atc cac Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His 625 630 635 640	1920
acg gag acc gcc agc tgg atg ttc ggc gtc ccc cgg gag gcc gtg gac Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp 645 650 655	1968
ccc ctg atg cgc cgg gcg gcc aag acc atc aac ttc ggg gtc ctc tac Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr 660 665 670	2016
ggc atg tcg gcc cac cgc ctc tcc cag gag cta gcc atc cct tac gag Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu 675 680 685	2064
gag gcc cag gcc ttc att gag cgc tac ttt cag agc ttc ccc aag gtg Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val 690 695 700	2112
cgg gcc tgg att gag aag acc ctg gag gag ggc agg agg cgg ggg tac Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr 705 710 715 720	2160
gtg gag acc ctc ttc ggc cgc cgc cgc tac gtg cca gac cta gag gcc Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala 725 730 735	2208
cgg gtg aag agc gtg cgg gag gcg gcc gag cgc atg gcc ttc aac atg Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met 740 745 750	2256
ccc gtc cag ggc acc gcc gcc gac ctc atg aag ctg gct atg gtg aag Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys 755 760 765	2304
ctc ttc ccc agg ctg gag gaa atg ggg gcc agg atg ctc ctt cag gtc Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val 770 775 780	2352
cac gac gag ctg gtc ctc gag gcc cca aaa gag agg gcg gag gcc gtg His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val 785 790 795 800	2400
gcc cgg ctg gcc aag gag gtc atg gag ggg gtg tat ccc ctg gcc gtg Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val 805 810 815	2448
ccc ctg gag gtg gag gtg ggg ata ggg gag gac tgg ctc tcc gcc aag Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys 820 825 830	2496
gag tgatag Glu	2505

<210> 132
 <211> 833
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 132
 Met Asn Ser Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu
 1 5 10 15
 Leu Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys
 20 25 30
 Gly Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe
 35 40 45
 Ala Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile
 50 55 60
 Val Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly
 65 70 75 80
 Gly Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln
 85 90 95
 Leu Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu
 100 105 110
 Glu Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys
 115 120 125
 Lys Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys
 130 135 140
 Asp Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu
 145 150 155 160
 Gly Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg
 165 170 175
 Pro Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp
 180 185 190
 Asn Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu
 195 200 205
 Leu Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg
 210 215 220
 Leu Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu
 225 230 235 240
 Lys Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu
 245 250 255
 Val Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala
 260 265 270

Phe Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu
275 280 285
Leu Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu
290 295 300
Gly Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala
305 310 315 320
Asp Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala
325 330 335
Pro Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu
340 345 350
Leu Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu
355 360 365
Pro Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser
370 375 380
Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr
385 390 395 400
Glu Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn
405 410 415
Leu Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg
420 425 430
Glu Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr
435 440 445
Gly Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val
450 455 460
Ala Gly Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly
465 470 475 480
His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe
485 490 495
Asp Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys
500 505 510
Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro
515 520 525
Ile Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser
530 535 540
Thr Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg
545 550 555 560
Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser
565 570 575
Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly
580 585 590
Gln Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val
595 600 605

Ala Leu Val Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser
 610 615 620
 Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His
 625 630 635 640
 Thr Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp
 645 650 655
 Pro Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr
 660 665 670
 Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu
 675 680 685
 Glu Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val
 690 695 700
 Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr
 705 710 715 720
 Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala
 725 730 735
 Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met
 740 745 750
 Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys
 755 760 765
 Leu Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val
 770 775 780
 His Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val
 785 790 795 800
 Ala Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val
 805 810 815
 Pro Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys
 820 825 830

Glu

<210> 133

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 133

aaaattcctt tctctttgcc ctttgcttcc

30

```

<210> 134
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<221> misc_feature
<222> (1)..(2)
<223> The residues at these positions are a
      2'deoxycytosine 5'-O-(1-Thiomonophosphate) .

<220>
<221> misc_feature
<222> (3)
<223> The residue at this position is a 2'deoxythymidine
      5'-O-(1-Thiomonophosphate) .

<220>
<221> misc_feature
<222> (4)..(5)
<223> The residues at these positions are a
      2'deoxyadenosine 5'-O-(1-Thiomonophosphate) .

<220>
<221> misc_feature
<222> (6)..(8)
<223> The residues at these positions are a
      2'deoxythymidine 5'-O-(1-Thiomonophosphate) .

<220>
<221> misc_feature
<222> (9)
<223> The residue at this position is a 2'deoxyguanosine
      5'-O-(1-Thiomonophosphate) .

<220>
<221> misc_feature
<222> (10)
<223> The residue at this position is a 2'deoxycytosine
      5'-O-(1-Thiomonophosphate) .

<220>
<223> Description of Artificial Sequence:  Synthetic

<400> 134
cctaatttgc cagttacaaa ataaacagcc c
31

<210> 135
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:  Synthetic

<400> 135
tgtggaattg tgagcgg
17

```

<210> 136
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 136
tggaggctct ccatcaaaaa c 21

<210> 137
<211> 296
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 137
tgtggaattg tgagcggata acaatttcac acaggaaaca gaccatggga gtgcagtttg 60
gtgattttat tccaaaaaat attatctcct ttgaagattt aaaagggaaa aaagtagcta 120
ttgatggaat gaatgcatta tatcagtttt taacatctat acgtttgaga gatggttctc 180
cattgagaaa tagaaaagga gagataacct cagcatataa cggagttttt tataaaacca 240
tacatttggt agagaatgat ataactccaa tctgggtttt tgatggagag cctcca 296

<210> 138
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 138
taatctgtat caggctg 17

<210> 139
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 139
gtttttgatg gagagcctcc a 21

<210> 140
<211> 889
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 140

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gtttttgatg gagagcctcc agaattcaaa aagaaagagc tcgaaaaaag aagagaagcg 60
agagaggaag ctgaagaaaa gtggagagaa gcacttgaaa aaggagagat agaggaagca 120
agaaaatatg cccaaagagc aaccagggtta aatgaaatgc tcatcgagga tgcaaaaaaa 180
ctcttagagc ttatgggaat tcctatagtt caagcaccta gcgagggaga ggcccaagct 240
gcatatatgg ccgcaaaggg gagcgtgtat gcatcggcta gtcaagatta cgattcccta 300
ctttttggag ctccaagact tgtagaaaac ttaacaataa caggaaaaag aaagttgcct 360
gggaaaaatg tctacgtcga gataaagccc gagttgataa ttttggagga agtactcaag 420
gaattaaagc taacaagaga aaagctcatt gaactagcaa tcctcgttgg aacagactac 480
aaccaggag gaataaaggg cataggcctt aaaaagctt tagagattgt tagacactca 540
aaagatccgc tagcaaagtt ccaaagcaa agcgatgtgg atttatatgc aataaaagag 600
ttcttcctaa acccaccagt cacagataac tacaatttag tgtggagaga tcccgcgaa 660
gaggaatac taaagttcct atgtgacgag catgacttta gtgaggaaag agtaaagaat 720
ggattagaga ggcttaagaa ggcaatcaaa agtggaaaac aatcaaccct tgaaagttgg 780
ttcaagagat aaccttaaag tctattgcaa tggtatactg acgcgctgca ggcattgcaag 840
cttggtgtgt ttggcggatg agagaagatt ttcagcctga tacagatta 889
```

<210> 141
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 141

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tgtggaattg tgagcggata acaatttcac acaggaaaca gaccatggga gtgcagtttg 60
gtgattttat tccaaaaaat attatctcct ttgaagattt aaaagggaaa aaagtagcta 120
ttgatggaat gaatgcatta tatcagtttt taacatctat acgtttgaga gatggttctc 180
cattgagaaa tagaaaagga gagataacct cagcatataa cggagttttt tataaaacca 240
tacatttggt agagaatgat ataactccaa tctgggtttt tgatggagag cctccagaat 300
tcaaaaagaa agagctcgaa aaaagaagag aagcgagaga ggaagctgaa gaaaagtgga 360
gagaagcact tgaaaaagga gagatagagg aagcaagaaa atatgcccaa agagcaacca 420
```

```

gggtaaatga aatgctcatc gaggatgcaa aaaaactcctt agagcttatg ggaattccta 480
tagttcaagc acctagcgag ggagaggccc aagctgcata tatggccgca aaggggagcg 540
tgtatgcacg ggctagtcaa gattacgatt cctactttt tggagctcca agacttggtta 600
gaaacttaac aataacagga aaaagaaagt tgcttgggaa aaatgtctac gtcgagataa 660
agcccgagtt gataattttg gaggaagtac tcaaggaatt aaagctaaca agagaaaagc 720
tcattgaact agcaatcctc gttggaacag actacaaccc aggaggaata aagggcatag 780
gccttaaaaa agcttttagag attggttagac actcaaaaga tccgctagca aagttccaaa 840
agcaaagcga tgtggattta tatgcaataa aagagttcctt cctaaaccca ccagtcacag 900
ataactacaa tttagtgtgg agagatcccg acgaagaggg aataactaaag ttcttatgtg 960
acgagcatga ctttagtgag gaaagagtaa agaattgatt agagaggctt aagaaggcaa 1020
tcaaaagtgg aaaacaatca acccttgaaa gttgggttcaa gagataacct taaagtctat 1080
tgcaatgtta tactgacgcg ctgcaggcat gcaagcttgg ctgttttggc ggatgagaga 1140
agattttcag cctgatacag atta 1164

```

<210> 142

<211> 296

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 142

```

tgtggaattg tgagcggata acaatttcac acaggaaaca gaccatgggt gtcccaattg 60
gtgagattat accaagaaaa gaaattgagt tagaaaacct atacgggaaa aaaatcgcaa 120
tcgacgctct taatgcaatc taccaatttt tgtccacaat aagacagaaa gatggaactc 180
cacttatgga ttcaaagggg agaataacct cccacctaag cgggctcttt tacaggacaa 240
taaacctaag ggaggctgga ataaaacctg tgtatgtttt tgatggagag cctcca 296

```

<210> 143

<211> 840

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 143

```

gtttttgatg gagagcctcc aaagttaaag gagaaaacaa ggaaagttag gagagagatg 60
aaagagaaag ctgaacttaa gatgaaagag gcaattaaaa aggaggattt tgaagaagct 120
gctaagtatg caaagagggg tagctatcta actccgaaaa tgggtgaaaa ctgcaaatat 180

```


ttgttaagtt tgatgggcat tccgtatggt gaagctccct ctgagggaga ggcacaagca 240
 agctatatgg caaagaaggg agatgtttgg gcagttgtaa gtcaagatta tgatgccttg 300
 ttatatggag ctccgagagt tgttagaaat ttaacaacta caaaggagat gccagaactt 360
 attgaattaa atgagggttt agaggattta agaatttctt tggatgattt gatagatata 420
 gccatattta tgggaactga ctataatcca ggaggagtta aaggaatagg atttaaaagg 480
 gcttatgaat tggttagaag tgggtgtagct aaggatgttt tgaaaaaaga ggttgaatac 540
 tacgatgaga ttaagaggat atttaaagag ccaaagggtta ccgataacta ttcattaagc 600
 ctaaaattgc cagataaaga gggaattata aaattcttag ttgatgaaaa tgactttaat 660
 tatgataggg ttaaaaagca tgttgataaa ctctataact taattgcaaa caaaactaag 720
 caaaaaacat tagatgcatg gtttaaataa tttatataat tttgtgggat gtcgacctgc 780
 aggcattgcaa gcttggctgt tttggcggat gagagaagat tttcagcctg atacagatta 840

<210> 144

<211> 1115

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 144

tgtggaattg tgagcggata acaatttcac acaggaaaca gaccatgggt gtcccaattg 60
 gtgagattat accaagaaaa gaaattgagt tagaaaacct atacgggaaa aaaatcgcaa 120
 tcgacgctct taatgcaatc taccaatttt tgtccacaat aagacagaaa gatggaactc 180
 cacttatgga ttcaaaggggt agaataacct cccacctaaag cgggctcttt tacaggacaa 240
 taaacctaat ggaggctgga ataaaacctg tgtatgtttt tgatggagag cctccaaagt 300
 taaaggagaa aacaaggaaa gttaggagag agatgaaaga gaaagctgaa cttaatgatga 360
 aagaggcaat taaaaggag gattttgaag aagctgctaa gtatgcaaag agggttagct 420
 atctaactcc gaaaatgggt gaaaactgca aatatttggt aagtttgatg ggcattccgt 480
 atgttgaagc tccctctgag ggagaggcac aagcaagcta tatggcaaag aaggagatg 540
 tttgggcagt tgtaagtcaa gattatgatg ccttggtata tggagctccg agagttgtta 600
 gaaatttaac aactacaaag gagatgccag aacttattga attaaatgag gttttagagg 660
 atttaagaat ttctttggat gatttgatag atatagccat atttatggga actgactata 720
 atccaggagg agttaagga ataggattta aaagggtta tgaattgggt agaagtgggt 780
 tagctaagga tgttttgaaa aaagaggttg aatactacga tgagattaag aggatattta 840
 aagagccaaa ggttaccgat aactattcat taagcctaaa attgccagat aaagagggaa 900

ttataaaatt cttagttgat gaaaatgact ttaattatga tagggttaaa aagcatgttg 960
ataaactcta taacttaatt gcaaacaaaa ctaagcaaaa aacattagat gcatggttta 1020
aataatttat ataattttgt gggatgtcga cctgcaggca tgcaagcttg gctgttttgg 1080
cggatgagag aagattttca gctgataca gatta 1115

<210> 145
<211> 386
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 145
tgtggaattg tgagcggata acaatttcac acaggaaaca gaccatgggt gtcccaattg 60
gtgagattat accaagaaaa gaaattgagt tagaaaacct atacgggaaa aaaatcgcaa 120
tcgacgctct taatgcaatc taccaatttt tgtccacaat aagacagaaa gatggaactc 180
cacttatgga ttcaaagggt agaataacct cccacctaag cgggctcttt tacaggacaa 240
taaacctaat ggaggctgga ataaaacctg tgtatgtttt tgatggagaa cctccagaat 300
tcaaaaagaa agagctcgaa aaaagaagag aagcgagaga ggaagctgaa gaaaagtgga 360
gagaagcact tgaaaaagga gagata 386

<210> 146
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 146
tacttagcag cttcttctat ctctcctttt tca 33

<210> 147
<211> 668
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 147
gaagaagctg ctaagtatgc aaagagggtt agctatctaa ctccgaaaat ggttgaaaac 60
tgcaaatatt tgtaagtatt gatgggcatt ccgtatgttg aagctccctc tgagggagag 120
gcacaagcaa gctatatggc aaagaaggga gatgtttggg cagttgtaag tcaagattat 180
gatgccttgt tatatggagc tccgagagtt gttagaaatt taacaactac aaaggagatg 240

ccagaactta ttgaattaaa tgaggtttta gaggatttaa gaatttcttt ggatgatttg 300
 atagatatag ccatatttat gggaactgac tataatccag gaggagttaa aggaatagga 360
 tttaaaaggg cttatgaatt ggtagaagt ggtgtagcta aggatgtttt gaaaaaagag 420
 gttgaatact acgatgagat taagaggata tttaaagagc caaagggttac cgataactat 480
 tcattaagcc taaaattgcc agataaagag ggaattataa aattcttagt tgatgaaaat 540
 gactttaatt atgatagggt taaaaagcat gttgataaac tctataactt aattgcaaac 600
 aaaactaagc aaaaaacatt agatgcatgg tttaaacacc accaccacca cactaactg 660
 cagcggta 668

<210> 148
 <211> 53
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 148
 taccgctgca gttagtgggtg gtgggtgggtg tgtttaaacc atgcatctaa tgt 53

<210> 149
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 149
 gaagaagctg ctaagta 17

<210> 150
 <211> 1054
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 150
 tgtggaattg tgagcggata acaatttcac acaggaaaca gaccatgggt gtcccaattg 60
 gtgagattat accaagaaaa gaaattgagt tagaaaacct atacgggaaa aaaatcgcaa 120
 tcgacgctct taatgcaatc taccaatttt tgtccacaat aagacagaaa gatggaactc 180
 cacttatgga ttcaaagggt agaataacct cccacctaa cggtctcttt tacaggacaa 240
 taaacctaat ggaggctgga ataaaacctg tgtatgtttt tgatggagaa cctccagaat 300
 tcaaaaagaa agagctcgaa aaaagaagag aagcgagaga ggaagctgaa gaaaagtgga 360

gagaagcact tgaaaaagga gagatagaag aagctgctaa gtatgcaaag agggttagct 420
 atctaactcc gaaaatgggt gaaaactgca aatatttggt aagtttgatg ggcattccgt 480
 atgttgaagc tccctctgag ggagaggcac aagcaagcta tatggcaaag aaggagatg 540
 tttgggcagt tgtaagtcaa gattatgatg ccttggtata tggagctccg agagttgtta 600
 gaaatttaac aactacaaag gagatgccag aacttattga attaaatgag gtttttagagg 660
 atttaagaat ttctttggat gatttgatag atatagccat atttatggga actgactata 720
 atccaggagg agttaaagga ataggattta aaagggtta tgaattgggt agaagtgggtg 780
 tagctaagga tgttttgaaa aaagaggttg aatactacga tgagattaag aggatattta 840
 aagagccaaa ggttaccgat aactattcat taagcctaaa attgccagat aaagagggaa 900
 ttataaaatt cttagttgat gaaaatgact ttaattatga taggggttaa aagcatgttg 960
 ataaactcta taacttaatt gcaaacaaaa ctaagcaaaa aacattagat gcatgggtta 1020
 aacaccacca ccaccaccac taactgcagc ggta 1054

<210> 151
 <211> 514
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 151
 tgtggaattg tgagcggata acaatttcac acaggaaaca gaccatggga gtgcagtttg 60
 gtgattttat tccaaaaaat attatctcct ttgaagattt aaaaggga aaagtagcta 120
 ttgatggaat gaatgcatta tatcagtttt taacatctat acgtttgaga gatgggtctc 180
 cattgagaaa tagaaaagga gagataacct cagcatataa cggagttttt tataaaacca 240
 tacatttggt agagaatgat ataactccaa tctgggtttt tgatggtgag ccaccaaagt 300
 taaaggagaa aacaaggaaa gttaggagag agatgaaaga gaaagctgaa cttaagatga 360
 aagaggcaat taaaaaggag gattttgaag aagctgctaa gtatgcaaag agggttagct 420
 atctaactcc gaaaatgggt gaaaactgca aatatttggt aagtttgatg ggcattccgt 480
 atgttgaagc tccctctgag ggagaggccc aagc 514

<210> 152
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 152
gcttgggcct ctccctc

17

<210> 153
<211> 667
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 153
gaggagagg cccaagctgc atatatggcc gcaaagggga gcgtgtatgc atcggctagt 60
caagattacg attccctact ttttggagct ccaagacttg ttagaaactt aacaataaca 120
ggaaaaagaa agttgcctgg gaaaaatgtc tacgtcgaga taaagcccgga gttgataatt 180
ttggaggaag tactcaagga attaaagcta acaagagaaa agctcattga actagcaatc 240
ctcgttggaa cagactacaa ccaggagga ataaagggca taggccttaa aaaagcttta 300
gagattgtta gacactcaaa agatccgcta gcaaagttcc aaaagcaaag cgatgtggat 360
ttatatgcaa taaaagagtt cttcctaaac ccaccagtca cagataacta caatttagtg 420
tggagagatc ccgacgaaga gggaatacta aagttcttat gtgacgagca tgactttagt 480
gaggaaagag taaagaatgg attagagagg cttaagaagg caatcaaaag tggaaaacaa 540
tcaacccttg aaagttgggtt caagagataa ccttaaagtc tattgcaatg ttatactgac 600
gcgctgcagg catgcaagct tggctgtttt ggcggatgag agaagatttt cagcctgata 660
cagatta 667

<210> 154
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 154
gaggagagg cccaagc

17

<210> 155
<211> 1164
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 155
 tgtggaattg tgagcggata acaatttcac acaggaaaca gaccatggga gtgcagtttg 60
 gtgattttat tccaaaaaat attatctcct ttgaagattt aaaagggaaa aaagtagcta 120
 ttgatggaat gaatgcatta tatcagtttt taacatctat acgtttgaga gatggttctc 180
 cattgagaaa tagaaaagga gagataacct cagcatataa cggagttttt tataaaacca 240
 tacatttggt agagaatgat ataactccaa tctgggtttt tgatggtgag ccaccaaagt 300
 taaaggagaa aacaaggaaa gttaggagag agatgaaaga gaaagctgaa cttaatgatga 360
 aagaggcaat taaaaaggag gattttgaag aagctgctaa gtatgcaaag agggtttagct 420
 atctaactcc gaaaatgggt gaaaactgca aatatttggt aagtttgatg ggcattccgt 480
 atgttgaagc tccctctgag ggagaggccc aagctgcata tatggccgca aaggggagcg 540
 tgtatgcata ggctagtcaa gattacgatt ccctactttt tggagctcca agacttgta 600
 gaaacttaac aataacagga aaaagaaagt tgctgggaa .aaatgtctac gtcgagataa 660
 agcccgagtt gataattttg gaggaagtac tcaaggaatt aaagctaaca agagaaaagc 720
 tcattgaact agcaatcctc gttggaacag actacaacc caggaggaata aagggcatag 780
 gccttaaaaa agcttttagag attgttagac actcaaaaga tccgctagca aagttccaaa 840
 agcaaagcga tgtggattta tatgcaataa aagagttctt cctaaacca ccagtcacag 900
 ataactacaa tttagtgtgg agagatcccg acgaagaggg aataactaaag ttcttatgtg 960
 acgagcatga ctttagtgag gaaagagtaa agaattgatt agagaggctt aagaaggcaa 1020
 tcaaaagtgg aaaacaatca acccttgaaa gttgggttcaa gagataacct taaagtctat 1080
 tgcaatgtta tactgacgag ctgcaggcat gcaagcttgg ctgttttggc ggatgagaga 1140
 agattttcag cctgatacag atta 1164

<210> 156
 <211> 514
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 156
 tgtggaattg tgagcggata acaatttcac acaggaaaca gaccatgggt gtcccaattg 60
 gtgagattat accaagaaaa gaaattgagt tagaaaacct atacgggaaa aaaatcgcaa 120
 tcgacgctct taatgcaatc taccaatttt tgtccacaat aagacagaaa gatggaactc 180
 cacttatgga ttcaaagggt agaataacct cccacctaag cgggctcttt tacaggacaa 240
 taaacctaat ggaggctgga ataaaacctg tgtatgtttt tgatggagaa cctccagaat 300
 tcaaaaagaa agagctcgaa aaaagaagag aagcgagaga ggaagctgaa gaaaagtgga 360

gagaagcact tgaaaaagga gagatagagg aagcaagaaa atatgcccac agagcaacca 420
 gggtaaatga aatgctcatc gaggatgcaa aaaaactctt agagcttatg ggaattccta 480
 tagttcaagc acctagcgag ggagaggccc aagc 514

<210> 157
 <211> 618
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 157
 gagggagagg cccaagcaag ctatatggca aagaaggag atgtttgggc agttgtaagt 60
 caagattatg atgccttggt atatggagct ccgagagttg ttagaaattt aacaactaca 120
 aaggagatgc cagaacttat tgaattaaat gaggttttag aggatttaag aatttccttg 180
 gatgatttga tagatatagc catatttatg ggaactgact ataatccagg aggagttaaa 240
 ggaataggat ttaaaagggc ttatgaattg gttagaagtg gtgtagctaa ggatgttttg 300
 aaaaaagagg ttgaatacta cgatgagatt aagaggatat ttaaagagcc aaagggtacc 360
 gataactatt cattaagcct aaaattgcca gataaagagg gaattataaa attcttagtt 420
 gatgaaaatg actttaatta tgataggggt aaaaagcatg ttgataaact ctataactta 480
 attgcaaaca aaactaagca aaaaacatta gatgcatggt ttaaataatt tatataattt 540
 tgtgggatgt cgacctgcag gcatgcaagc ttggctgttt tggcggatga gagaagattt 600
 tcagcctgat acagatta 618

<210> 158
 <211> 1115
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 158
 tgtggaattg tgagcggata acaatttcac acaggaaaca gaccatgggt gtcccaattg 60
 gtgagattat accaagaaaa gaaattgagt tagaaaacct atacgggaaa aaaatcgcaa 120
 tcgacgtctt taatgcaatc taccaatttt tgtccacaat aagacagaaa gatggaactc 180
 cacttatgga ttcaaagggg agaataacct cccacctaag cgggctcttt tacaggacaa 240
 taaacctaat ggaggctgga ataaaacctg tgtatgtttt tgatggagaa cctccagaat 300
 tcaaaaagaa agagctcgaa aaaagaagag aagcgagaga ggaagctgaa gaaaagtgga 360
 gagaagcact tgaaaaagga gagatagagg aagcaagaaa atatgcccac agagcaacca 420

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gggtaaatga aatgctcatc gaggatgcaa aaaaactctt agagcttatg ggaattccta 480
tagttcaagc acctagcgag ggagaggccc aagcaagcta tatggcaaag aaggagagatg 540
tttgggcagt tgtaagtcaa gattatgatg ccttggtata tggagctccg agagttgtta 600
gaaatttaac aactacaaag gagatgccag aacttattga attaaatgag gttttagagg 660
atttaagaat ttctttggat gatttgatag atatagccat atttatggga actgactata 720
atccaggagg agttaaagga ataggattta aaagggtta tgaattggtt agaagtgggtg 780
tagctaagga tgttttgaaa aaagagggtt aatactacga tgagattaag aggatattta 840
aagagccaaa ggttaccgat aactattcat taagcctaaa attgccagat aaagagggaa 900
ttataaaatt cttagttgat gaaaatgact ttaattatga tagggttaaa aagcatgttg 960
ataaactcta taacttaatt gcaaacaaaa ctaagcaaaa aacattagat gcatggttta 1020
aataatttat ataattttgt gggatgtcga cctgcaggca tgcaagcttg gctgtttttg 1080
cggatgagag aagattttca gcctgataca gatta 1115

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<210> 159

<211> 2505

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 159

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gtgcaggcgg tctacggctt cgccaagagc ctctcaagg ccctgaagga ggacgggtac 180
aaggccgtct tcgtggtctt tgacgccaag gccccctcct tccgccacga ggccctacgag 240
gcctacaagg cggggagggc cccgaccccc gaggacttcc cccggcagct cgccctcatc 300
aaggagctgg tggacctcct ggggtttacc cgctcgagg tccccggcta cgaggcggac 360
gacgttctcg ccaccctggc caagaaggcg gaaaaggagg ggtacgaggt gcgcctcctc 420
accgccgacc gcgacctcta ccaactcgtc tccgaccgag tcgcgctcct ccaccccgag 480
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ggggagaaga ccgccctcaa gctcctcaag gagtggggaa gcctggaaaa cctcctcaag 660
aacctggacc gggtaaagcc agaaaacgtc cgggagaaga tcaaggccca cctggaagac 720
ctcaggctct ccttgagct ctcccggtg cgcaccgacc tccccctgga ggtggacctc 780
gccaggggc gggagcccga ccgggagggg cttagggcct tcctggagag gctggagttc 840

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 ttggcctcga gggaggggct agacctcgtg cccggggacg acccatgct cctcgctac 1140
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 ctggaggccc tacgggaggc ccacccatc gtggagaaga tcctccagca ccgggagctc 1620
 accaagctca agaacaccta cgtggacccc ctccaagcc tcgtccaccg gaggacgggc 1680
 cgctccaca cccgcttcaa ccagacggcc acggccacgg ggaggcttag tagctccgac 1740
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 cacaccaga ccgcaagctg gatgttcggc gtccccccgg aggcctgga cccctgatg 1980
 cgccgggcgg ccaagacggt gaacttcggc gtctctacg gcatgtccgc ccataggctc 2040
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 gacctcatga agctcgccat ggtgaagctc ttccccgcc tccgggagat gggggccgc 2340
 atgtcctcc aggtccacga cgagctcctc ctggaggccc cccaagcgcg ggccgaggag 2400
 gtggcggctt tggccaagga ggcatggag aaggcctatc ccctcgccgt gccctggag 2460
 gtggaggtgg ggatggggga ggactggctt tccgccaagg gtttag 2505

<210> 160
 <211> 834
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 160

Met	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val	Leu	Leu
1				5					10					15	
Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu	Lys	Gly
			20					25					30		
Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly	Phe	Ala
			35				40					45			
Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala	Val	Phe
	50					55					60				
Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala	Tyr	Glu
	65				70					75					80
Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro	Arg	Gln
				85					90					95	
Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr	Arg	Leu
			100					105					110		
Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	Ala	Lys
		115					120					125			
Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	Asp	Arg
	130					135					140				
Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	Pro	Glu
	145				150					155					160
Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	Leu	Arg
			165					170						175	
Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	Ser	Asp
			180					185					190		
Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	Lys	Leu
		195					200					205			
Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	Asp	Arg
	210					215					220				
Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	Glu	Asp
	225				230					235					240
Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	Pro	Leu
			245						250					255	
Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	Leu	Arg
			260					265					270		
Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly
		275					280					285			

Leu Leu Glu Ala Pro Ala Pro Leu Glu Glu Ala Pro Trp Pro Pro Pro
 290 295 300
 Glu Gly Ala Phe Val Gly Phe Val Leu Ser Arg Pro Glu Pro Met Trp
 305 310 315 320
 Ala Glu Leu Lys Ala Leu Ala Ala Cys Arg Asp Gly Arg Val His Arg
 325 330 335
 Ala Ala Asp Pro Leu Ala Gly Leu Lys Asp Leu Lys Glu Val Arg Gly
 340 345 350
 Leu Leu Ala Lys Asp Leu Ala Val Leu Ala Ser Arg Glu Gly Leu Asp
 355 360 365
 Leu Val Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro
 370 375 380
 Ser Asn Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp
 385 390 395 400
 Thr Glu Asp Ala Ala His Arg Ala Leu Leu Ser Glu Arg Leu His Arg
 405 410 415
 Asn Leu Leu Lys Arg Leu Glu Gly Glu Glu Lys Leu Leu Trp Leu Tyr
 420 425 430
 His Glu Val Glu Lys Pro Leu Ser Arg Val Leu Ala His Met Glu Ala
 435 440 445
 Thr Gly Val Arg Arg Asp Val Ala Tyr Leu Gln Ala Leu Ser Leu Glu
 450 455 460
 Leu Ala Glu Glu Ile Arg Arg Leu Glu Glu Glu Val Phe Arg Leu Ala
 465 470 475 480
 Gly His Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu
 485 490 495
 Phe Asp Glu Leu Arg Leu Pro Ala Leu Gly Lys Thr Gln Lys Thr Gly
 500 505 510
 Lys Arg Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His
 515 520 525
 Pro Ile Val Glu Lys Ile Leu Gln His Arg Glu Leu Thr Lys Leu Lys
 530 535 540
 Asn Thr Tyr Val Asp Pro Leu Pro Ser Leu Val His Pro Arg Thr Gly
 545 550 555 560
 Arg Leu His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu
 565 570 575
 Ser Ser Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu
 580 585 590
 Gly Gln Arg Ile Arg Arg Ala Phe Val Ala Glu Ala Gly Trp Ala Leu
 595 600 605
 Val Ala Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu
 610 615 620

Ser Gly Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Lys Asp Ile
 625 630 635 640
 His Thr Gln Thr Ala Ser Trp Met Phe Gly Val Pro Pro Glu Ala Val
 645 650 655
 Asp Pro Leu Met Arg Arg Ala Ala Lys Thr Val Asn Phe Gly Val Leu
 660 665 670
 Tyr Gly Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr
 675 680 685
 Glu Glu Ala Val Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys
 690 695 700
 Val Arg Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Lys Arg Gly
 705 710 715 720
 Tyr Val Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Asn
 725 730 735
 Ala Arg Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn
 740 745 750
 Met Pro Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val
 755 760 765
 Lys Leu Phe Pro Arg Leu Arg Glu Met Gly Ala Arg Met Leu Leu Gln
 770 775 780
 Val His Asp Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala Glu Glu
 785 790 795 800
 Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro Leu Ala
 805 810 815
 Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu Ser Ala
 820 825 830

Lys Gly

<210> 161

<211> 2511

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 161

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 ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
 gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggcct gaaggaggac 180
 ggggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcg ccacgaggcc 240
 tacgaggcct acaaggcggg gagggccccg acccccagg acttccccg gcagctcgcc 300

ctcatcaagg agctggtgga cctcctgggg tttacccgcc tcgaggtccc cggtacgag 360
gcggacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcg 420
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cccgagggcc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
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gacctgccc aggggcggga gcccgaccgg gaggggctta gggccttccct ggagaggctg 840
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 gcccgcacgc tcctccaggt ccacgacgag ctctctctgg aggcccccca agcgcgggcc 2400
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
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<210> 162

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 162

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
	65				70					75					80
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
				85					90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
			100					105					110		
Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu
		115					120					125			
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala
	130					135					140				
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His
145					150					155					160
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly
				165					170					175	
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro
			180					185					190		
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu
		195					200					205			

Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu		
210						215					220						
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu		
225					230					235					240		
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu		
				245					250					255			
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly		
			260					265					270				
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu		
		275					280					285					
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro		
	290					295					300						
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro		
305					310					315					320		
Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Asp	Gly	Arg	Val		
				325					330					335			
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val		
			340					345					350				
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly		
		355					360					365					
Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu		
	370					375					380						
Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly		
385					390					395					400		
Glu	Trp	Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu		
				405					410					415			
His	Arg	Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp		
			420					425					430				
Leu	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met		
		435					440					445					
Glu	Ala	Thr	Gly	Val	Arg	Arg	Asp	Val	Ala	Tyr	Leu	Gln	Ala	Leu	Ser		
	450					455					460						
Leu	Glu	Leu	Ala	Glu	Glu	Ile	Arg	Arg	Leu	Glu	Glu	Glu	Val	Phe	Arg		
465					470					475				480			
Leu	Ala	Gly	His	Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg		
				485					490					495			
Val	Leu	Phe	Asp	Glu	Leu	Arg	Leu	Pro	Ala	Leu	Gly	Lys	Thr	Gln	Lys		
			500					505					510				
Thr	Gly	Lys	Arg	Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu		
		515					520					525					
Ala	His	Pro	Ile	Val	Glu	Lys	Ile	Leu	Gln	His	Arg	Glu	Leu	Thr	Lys		
	530					535					540						

Leu	Lys	Asn	Thr	Tyr	Val	Asp	Pro	Leu	Pro	Ser	Leu	Val	His	Pro	Arg	545	550	555	560
Thr	Gly	Arg	Leu	His	Thr	Arg	Phe	Asn	Gln	Thr	Ala	Thr	Ala	Thr	Gly	565	570	575	
Arg	Leu	Ser	Ser	Ser	Asp	Pro	Asn	Leu	Gln	Asn	Ile	Pro	Val	Arg	Thr	580	585	590	
Pro	Leu	Gly	Gln	Arg	Ile	Arg	Arg	Ala	Phe	Val	Ala	Glu	Ala	Gly	Trp	595	600	605	
Ala	Leu	Val	Ala	Leu	Asp	Tyr	Ser	Gln	Ile	Glu	Leu	Arg	Val	Leu	Ala	610	615	620	
His	Leu	Ser	Gly	Asp	Glu	Asn	Leu	Ile	Arg	Val	Phe	Gln	Glu	Gly	Lys	625	630	635	640
Asp	Ile	His	Thr	Gln	Thr	Ala	Ser	Trp	Met	Phe	Gly	Val	Pro	Pro	Glu	645	650	655	
Ala	Val	Asp	Pro	Leu	Met	Arg	Arg	Ala	Ala	Lys	Thr	Val	Asn	Phe	Gly	660	665	670	
Val	Leu	Tyr	Gly	Met	Ser	Ala	His	Arg	Leu	Ser	Gln	Glu	Leu	Ala	Ile	675	680	685	
Pro	Tyr	Glu	Glu	Ala	Val	Ala	Phe	Ile	Glu	Arg	Tyr	Phe	Gln	Ser	Phe	690	695	700	
Pro	Lys	Val	Arg	Ala	Trp	Ile	Glu	Lys	Thr	Leu	Glu	Glu	Gly	Arg	Lys	705	710	715	720
Arg	Gly	Tyr	Val	Glu	Thr	Leu	Phe	Gly	Arg	Arg	Arg	Tyr	Val	Pro	Asp	725	730	735	
Leu	Asn	Ala	Arg	Val	Lys	Ser	Val	Arg	Glu	Ala	Ala	Glu	Arg	Met	Ala	740	745	750	
Phe	Asn	Met	Pro	Val	Gln	Gly	Thr	Ala	Ala	Asp	Leu	Met	Lys	Leu	Ala	755	760	765	
Met	Val	Lys	Leu	Phe	Pro	Arg	Leu	Arg	Glu	Met	Gly	Ala	Arg	Met	Leu	770	775	780	
Leu	Gln	Val	His	Asp	Glu	Leu	Leu	Leu	Glu	Ala	Pro	Gln	Ala	Arg	Ala	785	790	795	800
Glu	Glu	Val	Ala	Ala	Leu	Ala	Lys	Glu	Ala	Met	Glu	Lys	Ala	Tyr	Pro	805	810	815	
Leu	Ala	Val	Pro	Leu	Glu	Val	Glu	Val	Gly	Met	Gly	Glu	Asp	Trp	Leu	820	825	830	
Ser	Ala	Lys	Gly													835			

<210> 163
<211> 2511
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic

<400> 163
atgaattccg aggcgatgct tccgctcttt gaacccaaag gccgggtcct cctggtggac 60
ggccaccacc tggcctaccg caccttcttc gccctgaagg gcctcaccac gagccggggc 120
gaaccggtgc aggcggtcta cggcttcgcc aagagcctcc tcaaggccct gaaggaggac 180
gggtacaagg ccgtcttcgt ggtctttgac gccaaaggccc cctccttcct ccacgaggcc 240
tacgaggcct acaaggcggg gagggccccg acccccaggg acttcccccg gcagctcgcc 300
ctcatcaagg agctggtgga cctcctgggg tttaccgcgc tcgaggtccc cggctacgag 360
gcggaacgacg ttctcgccac cctggccaag aaggcggaaa aggaggggta cgaggtgcgc 420
atcctcaccg ccgaccgcga cctctaccaa ctctctccg accgcgtcgc cgtcctccac 480
cccagggggc acctcatcac cccggagtgg ctttgggaga agtacggcct caggccggag 540
cagtgggtgg acttccgcgc cctcgtgggg gaccctccg acaacctccc cggggtcaag 600
ggcatcgggg agaagaccgc cctcaagctc ctcaaggagt ggggaagcct ggaaaacctc 660
ctcaagaacc tggaccgggt aaagccagaa aacgtccggg agaagatcaa ggcccacctg 720
gaagacctca ggctctcctt ggagctctcc cgggtgcgca ccgacctccc cctggagggtg 780
gacctcgccc aggggcggga gcccgaccgg gaggggctta gggccttcct ggagaggctg 840
gagttcggca gcctcctcca cgagttcggc ctcttgagg ccccgcccc cctggaggag 900
gccccctggc ccccgccgga aggggccttc gtgggcttcg tcctctcccg ccccgagccc 960
atgtgggcgg agcttaaagc cctggccgcc tgcaggagc gccgggtgca ccgggcagca 1020
gacccttggt cgggggctaaa ggacctcaag gaggtccggg gcctcctcgc caaggacctc 1080
gccgtcttgg cctcgaggga ggggctagac ctctgcccc gggacgacct catgctcctc 1140
gcctacctcc tggaccttc caacaccacc cccgaggggg tggcgcggcg ctacgggggg 1200
gagtggacgg aggacgccgc ccaccggggc ctctctcctg agaggctcca tcggaacctc 1260
cttaagcgcc tcgaggggga ggagaagctc ctttggctct accacgaggt ggaaaagccc 1320
ctctccccgg tcctggccca catggaggcc accggggtac ggcgggacgt ggcctacctt 1380
caggcccttt ccctggagct tgcggaggag atccgccgcc tcgaggagga ggtcttcgc 1440
ttggcgggcc accccttcaa cctcaactcc cgggaccagc tggaaagggg gctctttgac 1500
gagcttaggc ttcccgctt gggaagacg caaaagacag gcaagcgctc caccagcgcc 1560
gcggtgctgg aggccttacg ggaggccac cccatcgtgg agaagatcct ccagcaccgg 1620

gagctcacca agctcaagaa cacctacgtg gacccccctcc caagcctcgt ccacccgagg 1680
 acggggccgcc tccacacccg cttcaaccag acggccacgg ccacggggag gcttagtagc 1740
 tccgacccca acctgcagaa catccccgtc cgcacccccct tgggccagag gatccgccgg 1800
 gccttcgtgg ccgaggcggg ttgggcgttg gtggccctgg actatagcca gatagagctc 1860
 cgcgtcctcg cccacctctc cggggacgaa aacctgatca gggctctcca ggaggggaag 1920
 gacatccaca cccagaccgc aagctggatg ttcggcgtcc ccccgagggc cgtggacccc 1980
 ctgatgcgcc gggcggccaa gacggtgaac ttcggcgtcc tctacggcat gtccgcccac 2040
 aggctctccc aggagcttgc catcccctac gaggaggcgg tggcctttat agagcgctac 2100
 ttccaaagct tccccaaagg gcgggcctgg atagaaaaga ccctggagga ggggaggaag 2160
 cggggctacg tggaaaccct cttcggaaga aggcgctacg tgcccacact caacgcccgg 2220
 gtgaagagcg tcaggagggc cgcgagcgc atggccttca acatgcccgt ccagggcacc 2280
 gccgccgacc tcatgaagct cgccatggtg aagctcttcc cccgcctccg ggagatgggg 2340
 gcccgcatgc tctccaggt ccacaacgag ctctcctgg agggccccca agcgcgggcc 2400
 gaggaggtgg cggctttggc caaggaggcc atggagaagg cctatcccct cgccgtgccc 2460
 ctggaggtgg aggtggggat gggggaggac tggctttccg ccaagggtta g 2511

<210> 164

<211> 836

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 164

Met	Asn	Ser	Glu	Ala	Met	Leu	Pro	Leu	Phe	Glu	Pro	Lys	Gly	Arg	Val
1				5					10					15	
Leu	Leu	Val	Asp	Gly	His	His	Leu	Ala	Tyr	Arg	Thr	Phe	Phe	Ala	Leu
			20					25					30		
Lys	Gly	Leu	Thr	Thr	Ser	Arg	Gly	Glu	Pro	Val	Gln	Ala	Val	Tyr	Gly
		35					40					45			
Phe	Ala	Lys	Ser	Leu	Leu	Lys	Ala	Leu	Lys	Glu	Asp	Gly	Tyr	Lys	Ala
	50					55					60				
Val	Phe	Val	Val	Phe	Asp	Ala	Lys	Ala	Pro	Ser	Phe	Arg	His	Glu	Ala
	65				70					75				80	
Tyr	Glu	Ala	Tyr	Lys	Ala	Gly	Arg	Ala	Pro	Thr	Pro	Glu	Asp	Phe	Pro
			85						90					95	
Arg	Gln	Leu	Ala	Leu	Ile	Lys	Glu	Leu	Val	Asp	Leu	Leu	Gly	Phe	Thr
		100						105					110		

Arg	Leu	Glu	Val	Pro	Gly	Tyr	Glu	Ala	Asp	Asp	Val	Leu	Ala	Thr	Leu	115	120	125
Ala	Lys	Lys	Ala	Glu	Lys	Glu	Gly	Tyr	Glu	Val	Arg	Ile	Leu	Thr	Ala	130	135	140
Asp	Arg	Asp	Leu	Tyr	Gln	Leu	Val	Ser	Asp	Arg	Val	Ala	Val	Leu	His	145	150	155
Pro	Glu	Gly	His	Leu	Ile	Thr	Pro	Glu	Trp	Leu	Trp	Glu	Lys	Tyr	Gly	165	170	175
Leu	Arg	Pro	Glu	Gln	Trp	Val	Asp	Phe	Arg	Ala	Leu	Val	Gly	Asp	Pro	180	185	190
Ser	Asp	Asn	Leu	Pro	Gly	Val	Lys	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Leu	195	200	205
Lys	Leu	Leu	Lys	Glu	Trp	Gly	Ser	Leu	Glu	Asn	Leu	Leu	Lys	Asn	Leu	210	215	220
Asp	Arg	Val	Lys	Pro	Glu	Asn	Val	Arg	Glu	Lys	Ile	Lys	Ala	His	Leu	225	230	235
Glu	Asp	Leu	Arg	Leu	Ser	Leu	Glu	Leu	Ser	Arg	Val	Arg	Thr	Asp	Leu	245	250	255
Pro	Leu	Glu	Val	Asp	Leu	Ala	Gln	Gly	Arg	Glu	Pro	Asp	Arg	Glu	Gly	260	265	270
Leu	Arg	Ala	Phe	Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	275	280	285
Phe	Gly	Leu	Leu	Glu	Ala	Pro	Ala	Pro	Leu	Glu	Glu	Ala	Pro	Trp	Pro	290	295	300
Pro	Pro	Glu	Gly	Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Pro	Glu	Pro	305	310	315
Met	Trp	Ala	Glu	Leu	Lys	Ala	Leu	Ala	Ala	Cys	Arg	Asp	Gly	Arg	Val	325	330	335
His	Arg	Ala	Ala	Asp	Pro	Leu	Ala	Gly	Leu	Lys	Asp	Leu	Lys	Glu	Val	340	345	350
Arg	Gly	Leu	Leu	Ala	Lys	Asp	Leu	Ala	Val	Leu	Ala	Ser	Arg	Glu	Gly	355	360	365
Leu	Asp	Leu	Val	Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	370	375	380
Asp	Pro	Ser	Asn	Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	385	390	395
Glu	Trp	Thr	Glu	Asp	Ala	Ala	His	Arg	Ala	Leu	Leu	Ser	Glu	Arg	Leu	405	410	415
His	Arg	Asn	Leu	Leu	Lys	Arg	Leu	Glu	Gly	Glu	Glu	Lys	Leu	Leu	Trp	420	425	430
Leu	Tyr	His	Glu	Val	Glu	Lys	Pro	Leu	Ser	Arg	Val	Leu	Ala	His	Met	435	440	445

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Leu Gln Val His Asn Glu Leu Leu Leu Glu Ala Pro Gln Ala Arg Ala
 785 790 795 800
 Glu Glu Val Ala Ala Leu Ala Lys Glu Ala Met Glu Lys Ala Tyr Pro
 805 810 815
 Leu Ala Val Pro Leu Glu Val Glu Val Gly Met Gly Glu Asp Trp Leu
 820 825 830
 Ser Ala Lys Gly
 835

<210> 165
 <211> 350
 <212> DNA
 <213> Escherichia coli

<400> 165
 agagtttgat catggctcag attgaacgct ggcggcaggc ctaacacatg caagtcgaac 60
 ggtaacagga agaagcttgc ttctttgctg acgagtggcg gacgggtgag taatgtctgg 120
 gaaactgcct gatggagggg gataactact ggaaacggta gctaataccg cataacgtcg 180
 caagaccaa gagggggacc ttcgggcctc ttgccatcgg atgtgcccag atgggattag 240
 ctagtaggtg gggtaacggc tcacctaggc gacgatccct agctgggtctg agaggatgac 300
 cagccacact ggaactgaga cacggtccag actcctacgg gaggcagcag 350

<210> 166
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 166
 cacgaattcc gaggcgatgc ttccgctc 28

<210> 167
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 167
 tcgacgtcga ctaacccttg gcggaaagcc 30

<210> 168
 <211> 23
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 168
 gcatcgcctc ggaattcatg gtc 23

<210> 169
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 169
 caggaggagc tcgttggtgga cctgga 26

<210> 170
 <211> 26
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 170
 ccgtcaacat ttaccatggg tgcgga 26

<210> 171
 <211> 31
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 171
 ccgccacctc gtagtcgaca tccttttcgt g 31

<210> 172
 <211> 28
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 172
 ggggtgtccc atgggagtta aactcagg 28

<210> 173
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 173
 ctgaattctg cagaaaaagg gg 22

 <210> 174
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 174
 agagtttgat cctggctcag 20

 <210> 175
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 175
 ctgctgcctc ccgtaggagt 20

 <210> 176
 <211> 34
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 176
 ttttcgctgt ctcgctgaaa gcgagacagc gttt 34

 <210> 177
 <211> 59
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence: Synthetic

 <400> 177
 ttttcgctgt ctcgctgaaa gcgagacagc gaaagacgct cgtgaaacga gcgtctttg 59

<210> 178
 <211> 1011
 <212> DNA
 <213> Archaeoglobus fulgidus

<400> 178
 atgggtgcgg atattggtga cctctttgag agggaagagg tcgagcttga gtactttctca 60
 ggaaagaaaa ttgccgttga tgctttcaac acgctatacc agttcatctc gataataagg 120
 cagcctgacg gtacgccgtt aaaggactca cagggcagaa tcacctctca cctttccgga 180
 atcctataca gagtctccaa catggctgag gtgggaatca ggccggtggt tgtattcgac 240
 ggagagccac cggagttcaa gaaggctgaa attgaggaga ggaaaaagag aagggtgag 300
 gcagaggaga tgtggattgc ggctttgcag gcaggagata aggacgcgaa aaagtatgct 360
 caggctgcag ggaggggttga cgagtacatt gttgactccg caaagacgct ttttaagttac 420
 atggggattc cctttgtcga tgccccgtct gaaggagagg cgcaggctgc ttacatggca 480
 gcaaaaggcg atgtggagta cacaggaagc caggattacg attctctgct cttcggaagc 540
 ccgagactcg ccagaaatct cgcaataacg ggaaaaagga agcttcccgg caaaaatgtc 600
 tatgtggatg taaagccgga gataataatt ctggaaagca acctcaaaag gctggggttg 660
 acgagggagc agctcatcga catagcgatt ctggctggga cggactacaa tgaggggtgtg 720
 aagggtgtcg gcgtcaagaa ggctttgaac tacatcaaga cctacggaga tattttcagg 780
 gcactcaagg ctctgaaagt aaatattgac cacgtagagg agataaggaa tttcttctctg 840
 aatcctcctg tgactgacga ctacagaata gagttcaggg agcctgactt tgagaaggcc 900
 atcgagttcc tgtgcgagga gcacgacttc agcagggaga gggctcgagaa ggccttggag 960
 aagctcaaag ctctgaagtc aaccaggcc acgcttgaga ggtggttctg a 1011

<210> 179
 <211> 336
 <212> PRT
 <213> Archaeoglobus fulgidus

<400> 179
 Met Gly Ala Asp Ile Gly Asp Leu Phe Glu Arg Glu Glu Val Glu Leu
 1 5 10 15
 Glu Tyr Phe Ser Gly Lys Lys Ile Ala Val Asp Ala Phe Asn Thr Leu
 20 25 30
 Tyr Gln Phe Ile Ser Ile Ile Arg Gln Pro Asp Gly Thr Pro Leu Lys
 35 40 45
 Asp Ser Gln Gly Arg Ile Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
 50 55 60
 Val Ser Asn Met Val Glu Val Gly Ile Arg Pro Val Phe Val Phe Asp
 65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Ala Glu Ile Glu Glu Arg Lys Lys
 85 90 95
 Arg Arg Ala Glu Ala Glu Glu Met Trp Ile Ala Ala Leu Gln Ala Gly
 100 105 110
 Asp Lys Asp Ala Lys Lys Tyr Ala Gln Ala Ala Gly Arg Val Asp Glu
 115 120 125
 Tyr Ile Val Asp Ser Ala Lys Thr Leu Leu Ser Tyr Met Gly Ile Pro
 130 135 140
 Phe Val Asp Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met Ala
 145 150 155 160
 Ala Lys Gly Asp Val Glu Tyr Thr Gly Ser Gln Asp Tyr Asp Ser Leu
 165 170 175
 Leu Phe Gly Ser Pro Arg Leu Ala Arg Asn Leu Ala Ile Thr Gly Lys
 180 185 190
 Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Asp Val Lys Pro Glu Ile
 195 200 205
 Ile Ile Leu Glu Ser Asn Leu Lys Arg Leu Gly Leu Thr Arg Glu Gln
 210 215 220
 Leu Ile Asp Ile Ala Ile Leu Val Gly Thr Asp Tyr Asn Glu Gly Val
 225 230 235 240
 Lys Gly Val Gly Val Lys Lys Ala Leu Asn Tyr Ile Lys Thr Tyr Gly
 245 250 255
 Asp Ile Phe Arg Ala Leu Lys Ala Leu Lys Val Asn Ile Asp His Val
 260 265 270
 Glu Glu Ile Arg Asn Phe Phe Leu Asn Pro Pro Val Thr Asp Asp Tyr
 275 280 285
 Arg Ile Glu Phe Arg Glu Pro Asp Phe Glu Lys Ala Ile Glu Phe Leu
 290 295 300
 Cys Glu Glu His Asp Phe Ser Arg Glu Arg Val Glu Lys Ala Leu Glu
 305 310 315 320
 Lys Leu Lys Ala Leu Lys Ser Thr Gln Ala Thr Leu Glu Arg Trp Phe
 325 330 335

<210> 180

<211> 777

<212> DNA

<213> Methanobacterium thermoautotrophicum

<400> 180

atgggagtta aactcagga tgttgatca cccgcagga tacgccttga ggaccttagg 60

ggaagaacgg tcgcagtcga tgcagccaac acactctacc agttcctatc aagcataagg 120

cagagggatg gaacaccct catggattcc aggggtagag taacatcaca cctcagcggc 180

atactctaca ggacggccgc ggtcatggag agggagataa gggctcatata tgtcttcgat 240
 ggaaggtccc accacctcaa gggcgagacc gtgagcagga gggctgatat ccggaagaaa 300
 tctgaggttg agtgaagag ggccttgag gagggggaca ttgacagggc gaaaaaatat 360
 gctgtaaggt cctcaaggat gtcctcagaa atactggaga gttcaaagag gtccttgaa 420
 cttctgggaa taccctatgt acaggcacc ggtgaggggg aggctcaggc atcatacatg 480
 gttaagatgg gcgatgcatg ggccgtggca tcccaggact atgactgtct cctctttggc 540
 gcccgaaggg ttgtaaggaa cctcaccctc agcggaaaac ttgaggacc cgagatcatt 600
 gaactggagt ccaccctcag ggaactctca atcagccaca cacagctcgt ggatatggca 660
 ctactcgtcg ggactgactt caatgagggt gtaaagggga taggcgcaag gaggggactc 720
 aaactcatca gggagaaggg cgacattttc aaagtcatca gggaccttga agcttga 777

<210> 181
 <211> 258
 <212> PRT
 <213> Methanobacterium thermoautotrophicum

<400> 181
 Met Gly Val Lys Leu Arg Asp Val Val Ser Pro Arg Arg Ile Arg Leu
 1 5 10 15
 Glu Asp Leu Arg Gly Arg Thr Val Ala Val Asp Ala Ala Asn Thr Leu
 20 25 30
 Tyr Gln Phe Leu Ser Ser Ile Arg Gln Arg Asp Gly Thr Pro Leu Met
 35 40 45
 Asp Ser Arg Gly Arg Val Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
 50 55 60
 Thr Ala Ala Val Met Glu Arg Glu Ile Arg Val Ile Tyr Val Phe Asp
 65 70 75 80
 Gly Arg Ser His His Leu Lys Gly Glu Thr Val Ser Arg Arg Ala Asp
 85 90 95
 Ile Arg Lys Lys Ser Glu Val Glu Trp Lys Arg Ala Leu Glu Glu Gly
 100 105 110
 Asp Ile Asp Arg Ala Lys Lys Tyr Ala Val Arg Ser Ser Arg Met Ser
 115 120 125
 Ser Glu Ile Leu Glu Ser Ser Lys Arg Leu Leu Glu Leu Leu Gly Ile
 130 135 140
 Pro Tyr Val Gln Ala Pro Gly Glu Gly Glu Ala Gln Ala Ser Tyr Met
 145 150 155 160
 Val Lys Met Gly Asp Ala Trp Ala Val Ala Ser Gln Asp Tyr Asp Cys
 165 170 175
 Leu Leu Phe Gly Ala Pro Arg Val Val Arg Asn Leu Thr Leu Ser Gly
 180 185 190

Lys Leu Glu Asp Pro Glu Ile Ile Glu Leu Glu Ser Thr Leu Arg Glu
 195 200 205
 Leu Ser Ile Ser His Thr Gln Leu Val Asp Met Ala Leu Leu Val Gly
 210 215 220
 Thr Asp Phe Asn Glu Gly Val Lys Gly Ile Gly Ala Arg Arg Gly Leu
 225 230 235 240
 Lys Leu Ile Arg Glu Lys Gly Asp Ile Phe Lys Val Ile Arg Asp Leu
 245 250 255
 Glu Ala

<210> 182
 <211> 987
 <212> DNA
 <213> Methanobacterium thermoautotrophicum

<400> 182
 atgggagttta aactcagggga tgttgatatca ccccgagga .tacgccttga ggaccttagg 60
 ggaagaacgg tcgcagtcga tgcagccaac acactctacc agttcctatc aagcataagg 120
 cagaggggatg gaacacccct catggattcc aggggtagag taacatcaca cctcagcggc 180
 atactctaca ggacggccgc ggtcatggag agggagataa gggcatata tgtcttcgat 240
 ggaaggtccc accacctcaa gggcgagacc gtgagcagga gggctgatat ccggaagaaa 300
 tctgaggttg agtgaagag ggcccttgag gagggggaca ttgacagggc gagaaaatat 360
 gctgtaaggt cctcaaggat gtcctcagaa atactggaga gttcaaagag gctcctggaa 420
 cttctgggaa taccctatgt acaggcaccc ggtgaggggg aggctcaggc atcatacatg 480
 gttaagatgg gcgatgcatg ggccgtggca tcccaggact atgactgtct cctctttggc 540
 gcccgaaggg ttgtaaggaa ggtcacctc agcggaaaac ttgaggaccc ccacatcatt 600
 gaactggagt ccaccctcag ggccctctca atcagccaca cacagctcgt ggatatggca 660
 ctactcgtcg ggactgactt caatgagggt gtaaaggggt atggcgcaag gaggggactc 720
 aaactcatca gggagaaggg cgacattttc aaagtcatca gggaccttga agctgacata 780
 ggtggcgacc cccaggtcct caggaggatc tttctggagc cagaggtttc agaggactat 840
 gagatcaggt ggagaaaacc tgacgtggaa ggtgttatcg agttcctgtg cactgaacac 900
 ggcttttcag aggaccgtgt gagggatgca cttaaaaaat ttgaggggtgc atcctccacc 960
 cagaagagcc tggaggactg gttctga 987

<210> 183
 <211> 328
 <212> PRT
 <213> Methanobacterium thermoautotrophicum

<400> 183

Met Gly Val Lys Leu Arg Asp Val Val Ser Pro Arg Arg Ile Arg Leu
1 5 10 15
Glu Asp Leu Arg Gly Arg Thr Val Ala Val Asp Ala Ala Asn Thr Leu
20 25 30
Tyr Gln Phe Leu Ser Ser Ile Arg Gln Arg Asp Gly Thr Pro Leu Met
35 40 45
Asp Ser Arg Gly Arg Val Thr Ser His Leu Ser Gly Ile Leu Tyr Arg
50 55 60
Thr Ala Ala Val Met Glu Arg Glu Ile Arg Val Ile Tyr Val Phe Asp
65 70 75 80
Gly Arg Ser His His Leu Lys Gly Glu Thr Val Ser Arg Arg Ala Asp
85 90 95
Ile Arg Lys Lys Ser Glu Val Glu Trp Lys Arg Ala Leu Glu Glu Gly
100 105 110
Asp Ile Asp Arg Ala Arg Lys Tyr Ala Val Arg Ser Ser Arg Met Ser
115 120 125
Ser Glu Ile Leu Glu Ser Ser Lys Arg Leu Leu Glu Leu Leu Gly Ile
130 135 140
Pro Tyr Val Gln Ala Pro Gly Glu Gly Glu Ala Gln Ala Ser Tyr Met
145 150 155 160
Val Lys Met Gly Asp Ala Trp Ala Val Ala Ser Gln Asp Tyr Asp Cys
165 170 175
Leu Leu Phe Gly Ala Pro Arg Val Val Arg Lys Val Thr Leu Ser Gly
180 185 190
Lys Leu Glu Asp Pro His Ile Ile Glu Leu Glu Ser Thr Leu Arg Ala
195 200 205
Leu Ser Ile Ser His Thr Gln Leu Val Asp Met Ala Leu Leu Val Gly
210 215 220
Thr Asp Phe Asn Glu Gly Val Lys Gly Tyr Gly Ala Arg Arg Gly Leu
225 230 235 240
Lys Leu Ile Arg Glu Lys Gly Asp Ile Phe Lys Val Ile Arg Asp Leu
245 250 255
Glu Ala Asp Ile Gly Gly Asp Pro Gln Val Leu Arg Arg Ile Phe Leu
260 265 270
Glu Pro Glu Val Ser Glu Asp Tyr Glu Ile Arg Trp Arg Lys Pro Asp
275 280 285
Val Glu Gly Val Ile Glu Phe Leu Cys Thr Glu His Gly Phe Ser Glu
290 295 300

Asp Arg Val Arg Asp Ala Leu Lys Lys Phe Glu Gly Ala Ser Ser Thr
 305 310 315 320

Gln Lys Ser Leu Glu Asp Trp Phe
 325

<210> 184

<211> 340

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 184

Met Gly Val Gln Phe Gly Asp Phe Ile Pro Lys Asn Ile Ile Ser Phe
 1 5 10 15

Glu Asp Leu Lys Gly Lys Lys Val Ala Ile Asp Gly Met Asn Ala Leu
 20 25 30

Tyr Gln Phe Leu Thr Ser Ile Arg Leu Arg Asp Gly Ser Pro Leu Arg
 35 40 45

Asn Arg Lys Gly Glu Ile Thr Ser Ala Tyr Asn Gly Val Phe Tyr Lys
 50 55 60

Thr Ile His Leu Leu Glu Asn Asp Ile Thr Pro Ile Trp Val Phe Asp
 65 70 75 80

Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu
 85 90 95

Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly
 100 105 110

Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn
 115 120 125

Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile
 130 135 140

Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ala Tyr Met
 145 150 155 160

Ala Ala Lys Gly Ser Val Tyr Ala Ser Ala Ser Gln Asp Tyr Asp Ser
 165 170 175

Leu Leu Phe Gly Ala Pro Arg Leu Val Arg Asn Leu Thr Ile Thr Gly
 180 185 190

Lys Arg Lys Leu Pro Gly Lys Asn Val Tyr Val Glu Ile Lys Pro Glu
 195 200 205

Leu Ile Ile Leu Glu Glu Val Leu Lys Glu Leu Lys Leu Thr Arg Glu
 210 215 220

Lys Leu Ile Glu Leu Ala Ile Leu Val Gly Thr Asp Tyr Asn Pro Gly
 225 230 235 240
 Gly Ile Lys Gly Ile Gly Leu Lys Lys Ala Leu Glu Ile Val Arg His
 245 250 255
 Ser Lys Asp Pro Leu Ala Lys Phe Gln Lys Gln Ser Asp Val Asp Leu
 260 265 270
 Tyr Ala Ile Lys Glu Phe Phe Leu Asn Pro Pro Val Thr Asp Asn Tyr
 275 280 285
 Asn Leu Val Trp Arg Asp Pro Asp Glu Glu Gly Ile Leu Lys Phe Leu
 290 295 300
 Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu
 305 310 315 320
 Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser
 325 330 335
 Trp Phe Lys Arg
 340

<210> 185
 <211> 326
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 185
 Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu
 1 5 10 15
 Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile
 20 25 30
 Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met
 35 40 45
 Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg
 50 55 60
 Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp
 65 70 75 80
 Gly Glu Pro Pro Lys Leu Lys Glu Lys Thr Arg Lys Val Arg Arg Glu
 85 90 95
 Met Lys Glu Lys Ala Glu Leu Lys Met Lys Glu Ala Ile Lys Lys Glu
 100 105 110
 Asp Phe Glu Glu Ala Ala Lys Tyr Ala Lys Arg Val Ser Tyr Leu Thr
 115 120 125

Pro Lys Met Val Glu Asn Cys Lys Tyr Leu Leu Ser Leu Met Gly Ile
 130 135 140
 Pro Tyr Val Glu Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met
 145 150 155 160
 Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala
 165 170 175
 Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Thr Lys
 180 185 190
 Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg
 195 200 205
 Ile Ser Leu Asp Asp Leu Ile Asp Ile Ala Ile Phe Met Gly Thr Asp
 210 215 220
 Tyr Asn Pro Gly Gly Val Lys Gly Ile Gly Phe Lys Arg Ala Tyr Glu
 225 230 235 240
 Leu Val Arg Ser Gly Val Ala Lys Asp Val Leu Lys Lys Glu Val Glu
 245 250 255
 Tyr Tyr Asp Glu Ile Lys Arg Ile Phe Lys Glu Pro Lys Val Thr Asp
 260 265 270
 Asn Tyr Ser Leu Ser Leu Lys Leu Pro Asp Lys Glu Gly Ile Ile Lys
 275 280 285
 Phe Leu Val Asp Glu Asn Asp Phe Asn Tyr Asp Arg Val Lys Lys His
 290 295 300
 Val Asp Lys Leu Tyr Asn Leu Ile Ala Asn Lys Thr Lys Gln Lys Thr
 305 310 315 320
 Leu Asp Ala Trp Phe Lys
 325

<210> 186

<211> 332

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 186

Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu
 1 5 10 15
 Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile
 20 25 30
 Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met
 35 40 45
 Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg
 50 55 60

Thr	Ile	Asn	Leu	Met	Glu	Ala	Gly	Ile	Lys	Pro	Val	Tyr	Val	Phe	Asp	65	70	75	80
Gly	Glu	Pro	Pro	Glu	Phe	Lys	Lys	Lys	Glu	Leu	Glu	Lys	Arg	Arg	Glu	85	90	95	
Ala	Arg	Glu	Glu	Ala	Glu	Glu	Lys	Trp	Arg	Glu	Ala	Leu	Glu	Lys	Gly	100	105	110	
Glu	Ile	Glu	Glu	Ala	Ala	Lys	Tyr	Ala	Lys	Arg	Val	Ser	Tyr	Leu	Thr	115	120	125	
Pro	Lys	Met	Val	Glu	Asn	Cys	Lys	Tyr	Leu	Leu	Ser	Leu	Met	Gly	Ile	130	135	140	
Pro	Tyr	Val	Glu	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ser	Tyr	Met	145	150	155	160
Ala	Lys	Lys	Gly	Asp	Val	Trp	Ala	Val	Val	Ser	Gln	Asp	Tyr	Asp	Ala	165	170	175	
Leu	Leu	Tyr	Gly	Ala	Pro	Arg	Val	Val	Arg	Asn	Leu	Thr	Thr	Thr	Lys	180	185	190	
Glu	Met	Pro	Glu	Leu	Ile	Glu	Leu	Asn	Glu	Val	Leu	Glu	Asp	Leu	Arg	195	200	205	
Ile	Ser	Leu	Asp	Asp	Leu	Ile	Asp	Ile	Ala	Ile	Phe	Met	Gly	Thr	Asp	210	215	220	
Tyr	Asn	Pro	Gly	Gly	Val	Lys	Gly	Ile	Gly	Phe	Lys	Arg	Ala	Tyr	Glu	225	230	235	240
Leu	Val	Arg	Ser	Gly	Val	Ala	Lys	Asp	Val	Leu	Lys	Lys	Glu	Val	Glu	245	250	255	
Tyr	Tyr	Asp	Glu	Ile	Lys	Arg	Ile	Phe	Lys	Glu	Pro	Lys	Val	Thr	Asp	260	265	270	
Asn	Tyr	Ser	Leu	Ser	Leu	Lys	Leu	Pro	Asp	Lys	Glu	Gly	Ile	Ile	Lys	275	280	285	
Phe	Leu	Val	Asp	Glu	Asn	Asp	Phe	Asn	Tyr	Asp	Arg	Val	Lys	Lys	His	290	295	300	
Val	Asp	Lys	Leu	Tyr	Asn	Leu	Ile	Ala	Asn	Lys	Thr	Lys	Gln	Lys	Thr	305	310	315	320
Leu	Asp	Ala	Trp	Phe	Lys	His	His	His	His	His	His	His	His	His	His	325	330		

<210> 187

<211> 340

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

<400> 187

Met	Gly	Val	Gln	Phe	Gly	Asp	Phe	Ile	Pro	Lys	Asn	Ile	Ile	Ser	Phe
1				5					10					15	
Glu	Asp	Leu	Lys	Gly	Lys	Lys	Val	Ala	Ile	Asp	Gly	Met	Asn	Ala	Leu
			20					25					30		
Tyr	Gln	Phe	Leu	Thr	Ser	Ile	Arg	Leu	Arg	Asp	Gly	Ser	Pro	Leu	Arg
		35					40					45			
Asn	Arg	Lys	Gly	Glu	Ile	Thr	Ser	Ala	Tyr	Asn	Gly	Val	Phe	Tyr	Lys
	50					55					60				
Thr	Ile	His	Leu	Leu	Glu	Asn	Asp	Ile	Thr	Pro	Ile	Trp	Val	Phe	Asp
65					70					75					80
Gly	Glu	Pro	Pro	Lys	Leu	Lys	Glu	Lys	Thr	Arg	Lys	Val	Arg	Arg	Glu
				85					90					95	
Met	Lys	Glu	Lys	Ala	Glu	Leu	Lys	Met	Lys	Glu	Ala	Ile	Lys	Lys	Glu
			100					105					110		
Asp	Phe	Glu	Glu	Ala	Ala	Lys	Tyr	Ala	Lys	Arg	Val	Ser	Tyr	Leu	Thr
		115					120					125			
Pro	Lys	Met	Val	Glu	Asn	Cys	Lys	Tyr	Leu	Leu	Ser	Leu	Met	Gly	Ile
	130					135					140				
Pro	Tyr	Val	Glu	Ala	Pro	Ser	Glu	Gly	Glu	Ala	Gln	Ala	Ala	Tyr	Met
145					150					155					160
Ala	Ala	Lys	Gly	Ser	Val	Tyr	Ala	Ser	Ala	Ser	Gln	Asp	Tyr	Asp	Ser
				165					170					175	
Leu	Leu	Phe	Gly	Ala	Pro	Arg	Leu	Val	Arg	Asn	Leu	Thr	Ile	Thr	Gly
		180						185					190		
Lys	Arg	Lys	Leu	Pro	Gly	Lys	Asn	Val	Tyr	Val	Glu	Ile	Lys	Pro	Glu
		195					200					205			
Leu	Ile	Ile	Leu	Glu	Glu	Val	Leu	Lys	Glu	Leu	Lys	Leu	Thr	Arg	Glu
	210					215					220				
Lys	Leu	Ile	Glu	Leu	Ala	Ile	Leu	Val	Gly	Thr	Asp	Tyr	Asn	Pro	Gly
225					230					235					240
Gly	Ile	Lys	Gly	Ile	Gly	Leu	Lys	Lys	Ala	Leu	Glu	Ile	Val	Arg	His
				245					250					255	
Ser	Lys	Asp	Pro	Leu	Ala	Lys	Phe	Gln	Lys	Gln	Ser	Asp	Val	Asp	Leu
			260					265					270		
Tyr	Ala	Ile	Lys	Glu	Phe	Phe	Leu	Asn	Pro	Pro	Val	Thr	Asp	Asn	Tyr
		275					280					285			
Asn	Leu	Val	Trp	Arg	Asp	Pro	Asp	Glu	Glu	Gly	Ile	Leu	Lys	Phe	Leu
	290					295					300				

Cys Asp Glu His Asp Phe Ser Glu Glu Arg Val Lys Asn Gly Leu Glu
 305 310 315 320
 Arg Leu Lys Lys Ala Ile Lys Ser Gly Lys Gln Ser Thr Leu Glu Ser
 325 330 335
 Trp Phe Lys Arg
 340

<210> 188
 <211> 326
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic

<400> 188
 Met Gly Val Pro Ile Gly Glu Ile Ile Pro Arg Lys Glu Ile Glu Leu
 1 5 10 15
 Glu Asn Leu Tyr Gly Lys Lys Ile Ala Ile Asp Ala Leu Asn Ala Ile
 20 25 30
 Tyr Gln Phe Leu Ser Thr Ile Arg Gln Lys Asp Gly Thr Pro Leu Met
 35 40 45
 Asp Ser Lys Gly Arg Ile Thr Ser His Leu Ser Gly Leu Phe Tyr Arg
 50 55 60
 Thr Ile Asn Leu Met Glu Ala Gly Ile Lys Pro Val Tyr Val Phe Asp
 65 70 75 80
 Gly Glu Pro Pro Glu Phe Lys Lys Lys Glu Leu Glu Lys Arg Arg Glu
 85 90 95
 Ala Arg Glu Glu Ala Glu Glu Lys Trp Arg Glu Ala Leu Glu Lys Gly
 100 105 110
 Glu Ile Glu Glu Ala Arg Lys Tyr Ala Gln Arg Ala Thr Arg Val Asn
 115 120 125
 Glu Met Leu Ile Glu Asp Ala Lys Lys Leu Leu Glu Leu Met Gly Ile
 130 135 140
 Pro Ile Val Gln Ala Pro Ser Glu Gly Glu Ala Gln Ala Ser Tyr Met
 145 150 155 160
 Ala Lys Lys Gly Asp Val Trp Ala Val Val Ser Gln Asp Tyr Asp Ala
 165 170 175
 Leu Leu Tyr Gly Ala Pro Arg Val Val Arg Asn Leu Thr Thr Thr Lys
 180 185 190
 Glu Met Pro Glu Leu Ile Glu Leu Asn Glu Val Leu Glu Asp Leu Arg
 195 200 205

Ile	Ser	Leu	Asp	Asp	Leu	Ile	Asp	Ile	Ala	Ile	Phe	Met	Gly	Thr	Asp
210						215					220				
Tyr	Asn	Pro	Gly	Gly	Val	Lys	Gly	Ile	Gly	Phe	Lys	Arg	Ala	Tyr	Glu
225					230					235					240
Leu	Val	Arg	Ser	Gly	Val	Ala	Lys	Asp	Val	Leu	Lys	Lys	Glu	Val	Glu
				245					250					255	
Tyr	Tyr	Asp	Glu	Ile	Lys	Arg	Ile	Phe	Lys	Glu	Pro	Lys	Val	Thr	Asp
			260					265					270		
Asn	Tyr	Ser	Leu	Ser	Leu	Lys	Leu	Pro	Asp	Lys	Glu	Gly	Ile	Ile	Lys
		275					280					285			
Phe	Leu	Val	Asp	Glu	Asn	Asp	Phe	Asn	Tyr	Asp	Arg	Val	Lys	Lys	His
	290					295					300				
Val	Asp	Lys	Leu	Tyr	Asn	Leu	Ile	Ala	Asn	Lys	Thr	Lys	Gln	Lys	Thr
305					310					315					320
Leu	Asp	Ala	Trp	Phe	Lys										
				325											